

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:51:02 ; Search time 14.5 seconds  
(without alignments)  
798.519 Million cell updates/sec

Title: US-09-724-583-2  
Perfect score: 818  
Sequence: 1 MCSLPMARYIIKYADQKAL.....QLTKSEPSARTKFFEQSW 152

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	283	34.6	155	JC7104	interleukin-1 rece
2	260.5	31.8	178	C40956	interleukin-1 rece
3	257.5	31.5	178	A44610	interleukin-1 rece
4	241	29.5	177	A54377	interleukin-1 rece
5	238.5	29.2	177	A30368	interleukin-1 rece
6	238.5	29.2	180	A39386	interleukin-1 rece
7	137.5	16.8	267	S38373	interleukin-1 beta
8	134.5	16.4	267	JN0724	interleukin-1 beta
9	132	16.1	266	S23010	interleukin-1 beta
10	124.5	15.2	269	I55969	interleukin-1 beta
11	117	14.3	266	ICB01B	interleukin-1 beta
12	110.5	13.5	268	A30584	interleukin-1 beta
13	104.5	12.8	269	ICBU1B	interleukin-1 beta
14	92	11.2	214	JC5646	interleukin-1 beta
15	89	10.9	3623	T09456	intrinsc factor-B
16	84.5	10.3	299	I49264	ubiquitinating enz
17	80	9.8	381	A75490	probable transamin
18	80	9.8	1092	S42798	fibronectin-bindin
19	76.5	9.4	520	A46661	leukotriene B4 ome
20	76	9.3	463	S44267	sulfate adenylyltr
21	76	9.3	1117	S33851	fibronectin-kidney
22	71.5	8.7	4302	A38971	polycystic kidney
23	71	8.7	599	I53395	antigen LEC-A - mo
24	71	8.7	7962	I38346	elastic titin - hu
25	70.5	8.6	927	F0WSTA	retrovirus-related
26	70	8.6	263	C83616	beta-ketoadipate e
27	70	8.6	331	E75067	aminopeptidase m42
28	70	8.6	348	C69399	N5,N10-methylenete
29	69.5	8.5	465	E71409	sulfate adenylyltr

30 59.5 8.5 532 2 882354 deoxycytidylate de  
31 69 8.4 339 2 S09264 ig alpha chain c r  
32 69 8.4 355 2 T47147 hypothetical prote  
33 69 8.4 520 2 S45702 leukotriene-B4 20-  
34 69 8.4 700 2 A84243 phosphoribosylform  
35 68.5 8.4 256 2 T12999 aquaporin homolog  
36 68.5 8.4 450 2 T45573 anthranilate N-hyd  
37 68.5 8.4 557 4 EBRWMS iGE-binding protei  
38 68.5 8.4 656 2 E96713 hypothetical prote  
39 68.5 8.4 729 2 JC5812 norbin - rat  
40 68.5 8.4 892 1 S42228 replication licens  
41 67.5 8.3 2403 2 T30875 PRP8 protein homol  
42 67 8.2 398 2 F75417 L-sorboseone dehyd  
43 67 8.2 622 2 T51223 hypothetical prote  
44 67 8.2 665 2 H69101 archaeosine tRNA-r  
45 67 8.2 832 2 S41889 beta-galactosidase

ALIGNMENTS

RESULT 1  
JC7104  
interleukin-1 receptor antagonist - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: JC7104  
R:Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford  
Biochem. Biophys. Res. Commun. 263, 702-706, 1999  
A:Title: IL1HV1: A novel interleukin-1 receptor antagonist gene.  
A:Reference number: JC7104; MUID:99443727  
A:Accession: JC7104  
A:Molecule type: mRNA  
A:Residues: 1-155 <NUL>  
A:Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805  
C:Genetics:  
A:Gene: il1h1  
A:Map position: 2q14  
C:Keywords: macrophage

Query Match 34.6%; Score 283; DB 2; Length 155;  
Best Local Similarity 45.7%; Pred. No. 8.3e-22;  
Matches 63; Conservative 20; Mismatches 49; Indels 6; Gaps 3;  
QY 18 KALYTRDGLLVGDPVADNCC-AEKICTLPNRGLDRTKVPFLIGIGGSRGLACVETEFG 76  
DB 17 KVLYLHNNQLLAGLHAGKVIKGEISWPNRWLDASLSPVILGVQGSQCLSCGVQE- 75  
QY 77 PSLOLEDVNEELYKGGEEATFTFFOSSGSFRLLEAAAWFQWFLCGPAPQPVLTK 136  
DB 76 PTUTLEPVLNIMELYLGAKESKFTFYRDMGLTSSFSAAYPGWFLCTVPADQPVRLTK 135

QY 137 ESE-----PSARTKFFEQ 150  
DB 136 LPENGGNAPITDFVFOQ 153

RESULT 2  
C40956  
interleukin-1 receptor antagonist precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 16-Jul-1999  
C:Accession: C40956  
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Helindal, P.; Brandhuber, B.J.; Thomps  
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991  
A:Title: Interleukin-1 receptor antagonist is a member of the interleukin 1 gene fami  
A:Reference number: A40956; MUID:91271363  
A:Accession: C40956  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-178 <EIS>  
A:Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929



QY	16	DOKALYTRDGLLVGDPVADNC-CAEKICTLPNRLDRTKVPFIPLIGIOGSRCLACVETE	74
		:    :    :    :    :    :    :    :    :    :    :    :    :    :    :	
Db	44	NKFTYLNNQLVAGYLOGPNVNLEKIIDVVPIE-----PHALFLGIHGGMKLCSCKVKG	98
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
QY	75	EGPSIQLEDVNIIELYKGEAEATRTFFQSSSGSAFRLAAAWPGWFLCGPAEQPQVOL	134
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
Db	99	DETRLQLEAVNTDLSENKKDKRFAIRSDSGPTTFSESAACPWFLECTAMEADQPVS	158
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
QY	135	TKESEPSAR-TKVFPEQ	150
		:     :	
Db	159	TNMPDEGVWVKFYFOR	175
		:     :	
RESULT	6		
A39386			
Interleukin-1 receptor antagonist, long intracellular splice form - human			
N:Contains: interleukin-1 receptor antagonist, short intracellular splice form			
C:Species: Homo sapiens (man)			
C>Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000			
C:Accession: I37893; A39386			
R:Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani, J.; Exp. Med. 182, 623-628, 1995			
A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor			
A:Reference number: I37893; MUID:9535865			
A:Accession: I37893			
A>Status: translated from GB/EMBL/DDBJ			
A:Molecule type: mRNA			
A:Residues: 1-180 <RES>			
A:Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PTD:g1008971			
R:Hasilik, S.; Martin, G.; Van der, L.; Morris, J.; Pearce, A.; Bigler, C.F.; Jaffe, G.			
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991			
A:Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor an			
A:Reference number: A39386; MUID:91219436			
A:Accession: A39386			
A:Molecule type: mRNA			
A:Residues: 1-3,25-180 <HAS>			
A:Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292			
C:Comment: For an alternative splice form, see PIR:A30368			
C:Genetics:			
A:Gene: GDB:ILLRN			
A:Cross-references: GDB:I25897; OMIM:I47679			
A:Map position: 2q14.2-2q14.2			
C:Superfamily: Interleukin-1			
C:Keywords: alternative splicing; cytokine receptor			
F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #s			
F:1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f			
Query Match	29.2%	Score 238.5; DB 2; Length 180;	
Best Local Similarity	40.9%;	Pred. No. 3.7e-17;	
Matches	56; Conservative	16; Mismatches 56; Indels 7; Gaps 3;	
QY	16	DOKALYTRDGLLVGDPVADNC-CAEKICTLPNRLDRTKVPFIPLIGIOGSRCLACVETE	74
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
Db	47	NKFTYLNNQLVAGYLOGPNVNLEKIIDVVPIE-----PHALFLGIHGGMKLCSCKVKG	101
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
QY	75	EGPSIQLEDVNIIELYKGEAEATRTFFQSSSGSAFRLAAAWPGWFLCGPAEQPQVOL	134
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
Db	102	DETRLQLEAVNTDLSENKKDKRFAIRSDSGPTTFSESAACPWFLECTAMEADQPVS	161
		:    :    :    :    :    :    :    :    :    :    :    :    :    :	
QY	135	TKESEPSAR-TKVFPEQ	150
		:     :	
Db	162	TNMPDEGVWVKFYFOR	178
		:     :	
RESULT	7		
S38373			
interleukin-1 beta precursor - pig			
C:Species: Sus scrofa domestica (domestic pig)			
C>Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999			
C:Accession: S38373			
R:Van den Broeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.;			

Eur. J. Biochem. 217, 45-52, 1993  
A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetically  
A:Reference number: S38373; MUID:94039070  
A:Accession: S38373  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-267 <VAN>  
A:Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900  
C:Genetics:  
C:Introns: 16/2; 33/3; 99/1; 154/1; 197/3  
C:Superfamily: interleukin-1

Query Match 16.8%; Score 137.5; DB 2; Length 267;  
Best Local Similarity 32.3%; Pred. No. 1.4e-06;  
Matches 31; Conservative 20; Mismatches 44; Indels 1; Gaps 1;

QY 54 KVPFLIGGSRCLACVETEGPSIQLEDVNIIEELKGGEEATRTFFQSSGSAFRL 113  
169 KIPVTIGIKGNLYSCVMKDDPTQLQLEDVD-PKSPKRDMEKRFVFKTEIKNRVEFE 227  
114 AAAMPWFCLGPAEPQPVOLTKSEPSARTKTFYE 149  
228 SALYPNWIYSTQAEQKPVPLGNSGRQDITDTME 263

Db

RESULT 8  
JN0724  
Interleukin-1 beta precursor - pig  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 14-Jul-1994 #sequence\_revision 22-Nov-1996 #text\_change 22-Jun-1999  
C:Accession: JN0724  
R:Huetner, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.  
Gene 129, 285-289, 1993  
A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be  
A:Reference number: JN0724; MUID:93314975  
A:Accession: JN0724  
A:Molecule type: mRNA  
A:Residues: 1-267 <HUE>  
A:Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608  
A:Experimental source: alveolar macrophage  
C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes i  
ved form of interleukin-1-beta, unlike interleukin-1-alpha, is inactive.  
C:Comment: Interleukin-1-beta precursor is less heavily myristoylated than interleukin-1a  
Superfamily: Interleukin-1  
Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag  
F:77/Binding site: myristate (lys) (covalent) #status predicted

Query Match 16.4%; Score 134.5; DB 1; Length 267;  
Best Local Similarity 31.2%; Pred. No. 2.8e-06;  
Matches 30; Conservative 20; Mismatches 45; Indels 1; Gaps 1;

QY 54 KVPFLIGGSRCLACVETEGPSIQLEDVNIIEELKGGEEATRTFFQSSGSAFRL 113  
169 KIPVTIGIKGNLYSCVMKDDPTQLQLEDVD-PKSPKRDMEKRFVFKTEIKNRVEFE 227  
114 AAAMPWFCLGPAEPQPVOLTKSEPSARTKTFYE 149  
228 SALYPNWIYSTQAEQKPVPLGNSGRQDITDTME 263

Db

RESULT 9  
S23010  
Interleukin-1 beta precursor - sheep  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 08-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Oct-1999  
C:Accession: S23010; S43047; S13092; B61246  
R:Seow, H.F.; Rotheil, J.S.; David, M.J.; Wood, P.R.

DNA Seq. 1, 423-426, 1991  
A:Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.  
A:Reference number: S23010; MUID:92119335  
A:Accession: S23010  
A:Molecule type: mRNA  
A:Residues: 1-266 <SEO>  
A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809  
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an a  
R:Sargan, D.R.  
submitted to the EMBL Data Library, May 1992  
A:Reference number: S43047  
A:Accession: S43047  
A:Molecule type: mRNA  
A:Residues: 1-13, 'C', '15-54, 'K', '56-63, 'A', '65-144, 'L', '146-266 <SAR>  
A:Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274  
R:Fiskerstrand, C.; Sargan, D.  
Nucleic Acids Res. 18, 7165, 1990  
A:Title: Nucleotide sequence of ovine Interleukin-1 beta.  
A:Reference number: S13092; MUID:91088326  
A:Accession: S13092  
A:Molecule type: mRNA  
A:Residues: 1-13, 'C', '15-54, 'K', '56-61, 'S', '63, 'A', '65-144, 'L', '146-266 <FIS>  
A:Cross-references: EMBL:X54796  
A:Note: the authors translated the codon AGT for residue 62 as Arg  
R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.  
Immunology 74, 453-460, 1991  
A:Title: Molecular cloning and characterization of ovine IL-lalpha and IL-1beta.  
A:Reference number: A61246; MUID:92120716  
A:Accession: B61246  
A:Molecule type: mRNA  
A:Residues: 1-144, 'L', '146-266 <AND>  
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea  
ved form of interleukin-1-beta, unlike interleukin-1-alpha, is inactive.  
C:Comment: Interleukin-1-beta precursor is less heavily myristoylated than interleukin  
C:Genetics:  
A:Gene: IL-1-beta  
C:Superfamily: Interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen  
F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 16.1%; Score 132; DB 1; Length 266;  
Best Local Similarity 25.4%; Pred. No. 5.1e-06;  
Matches 34; Conservative 28; Mismatches 44; Indels 28; Gaps 3;

QY 16 DQKALYTRDQQLLVGDPVADNCCAEKICTLPNRLDR-----TKVPFLG 60  
127 EOKSL-----VLDSPCVLKALHLPSEMSREVVFQGEERDNKIPVALG 174  
61 IQGSRCLACVETEGPSIQLEDVNIIEELKGGEEATRTFFQSSGSAFRLAAAPGW 120  
175 IRDNLYLSCVKKGDDPTQLQLEDVD-PKVYPRKRMKEKRFVFKTEIKNVFEFSLPNW 233

Db

QY 121 FLCGPAEPQPVOL 134  
YISTQIEEKPVFL 247

Db

RESULT 10  
155969  
Interleukin-1 beta precursor - mouse  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Mus musculus (house mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 22-Nov-1996 #text\_change 22-Jun-1999  
C:Accession: 155969; A24719; S13029  
R:Gray, P.W.; Glaister, D.; Chen, E.; Gooddel, D.V.; Pennica, D.  
J. Immunol. 137, 3644-3648, 1986  
A:Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for  
A:Reference number: 155969; MUID:87058957  
A:Accession: 155969  
A>Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-269 <RES>

```

A:Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R:Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Falla, E.; Melll, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A:Title: The murine interleukin 1-beta gene: structure and evolution.
A:Reference number: A24719; MUID:87117546
A:Accession: A24719
A:Molecule type: mRNA
A:Residues: 1-269 <TEL>
A:Cross-references: GB:X04964; NID:g52666; PIDN:CAA2837.1; PID:g52667
R:Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColi, A.S.; Geoghegan, K.F.; Otterness, I.
FEBS Lett. 278, 98-102, 1991
A:Title: Reduction of biological activity of murine recombinant interleukin-1beta by sequestration of the protein.
A:Reference number: S13029; MUID:91130610
A:Accession: S13029
A:Status: preliminary
A:Molecule type: protein
A:Residues: 118-269 <DAU>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1-alpha.
C:Genetics:
Gene: il-1-beta
Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:118-269/Product: interleukin-1 beta #status experimental <ILL>

Query Match 15.2%; Score 124.5; DB 1; Length 269;
Best Local Similarity 24.4%; Pred. No. 3.1e-05;
Matches 39; Conservative 28; Mismatches 52; Indels 41; Gaps 5;

QY 1 MCSLPMAR-VYIKYADOKALYTRD-----GQ-----LLVGDPPADNCC 38
DQ 115 VCDVPIRLHVLRLDEQKSLVSDPYELKHLNGQINQVYFSFQGEPSND--- 171
Db 115 VCDVPIRLHVLRLDEQKSLVSDPYELKHLNGQINQVYFSFQGEPSND--- 171
QY 39 AEKICTLPNGLDRTKVPFLGTOGRCACVETEGPSLOLEDVNIIEELKGGEEATR 98
DQ 172 -----KIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKR 215
Db 172 -----KIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKR 215
QY 99 FTFQSSGSAFLRLEAAWPGFLGPAEPQVPQVLTRES 138
DQ 216 FVFNKKIEVSKVEFAEPFNWYISTSOAEHKPVFLGNNS 255
Db 216 FVFNKKIEVSKVEFAEPFNWYISTSOAEHKPVFLGNNS 255

RESULT 11
ICHO1B
interleukin-1 beta precursor - bovine
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
A:Accession: J10010; S01380
A:Reference number: A94695; MUID:89318652
A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin 1-beta.
Mol. Immunol. 25, 429-437, 1988
A:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 13.5%; Score 110.5; DB 1; Length 268;
Best Local Similarity 30.6%; Pred. No. 0.00084;
Matches 26; Conservative 16; Mismatches 42; Indels 1; Gaps 1;

QY 54 KVPFIFIGGSRCLACVETEGPSLOLEDVNIIEELKGGEEATRFTFFQSSGAPRL 113
DQ 170 KIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKRFTFNKIDKLEFE 228
Db 170 KIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKRFTFNKIDKLEFE 228
QY 114 AAAMPGWFLCGPAEPQVPQVLTRES 138
DQ 229 SAQFPNWKYISTSOAEHKPVFLGNNS 253
Db 229 SAQFPNWKYISTSOAEHKPVFLGNNS 253

RESULT 13
ICHO1B
interleukin-1 beta precursor [validated] - human
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 14.3%; Score 117; DB 1; Length 266;
Best Local Similarity 29.5%; Pred. No. 0.00018;
Matches 26; Conservative 24; Mismatches 36; Indels 2; Gaps 2;

QY 48 RGLDR-TKVPFIFIGGSRCLACVETEGPSLOLEDVNIIEELKGGEEATRFTFFQSS 106
DQ 161 QGEERDNKIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKRFTFNKIDKLEFE 219
Db 161 QGEERDNKIPVALGKGNLYLSCVMKDGDTPTLQLESDVPKQ-YPKKMKRFTFNKIDKLEFE 219
QY 107 GSAPRLEAAWPGFLGPAEPQVPQVLTRES 134
DQ 220 KNTVEFESVLYPNWYISTSOAEHKPVFL 247
Db 220 KNTVEFESVLYPNWYISTSOAEHKPVFL 247

RESULT 12
A30584
interleukin-1 beta precursor - rabbit
N:Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
A:Accession: A27714; A30584; J00082; A32166
R:Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A:Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating factor.
A:Reference number: A27714; MUID:88134238
A:Accession: A27714
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-268 <MOR>
R:Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello
J. Immunol. 142, 2299-2306, 1989
A:Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A:Reference number: A30584; MUID:89176242
A:Accession: A30584
A:Molecule type: mRNA
A:Residues: 1-268 <CAN>
A:Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R:Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A:Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A:Reference number: A94230; MUID:89315718
A:Accession: J00082
A:Molecule type: mRNA
A:Residues: 1-268 <YOU>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin 1-alpha.
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:117-268/Product: interleukin-1 beta #status predicted <ILB>

```

A:Reference number: A48293; MUID:93348250  
A:Contents: annotation; myristylation of lysines  
R:Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A:Title: The role of arginine residues in interleukin 1 receptor binding.  
A:Reference number: S19608; MUID:92110334  
A:Contents: annotation; type 1 IL-1 receptor interaction site  
A>Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
R:Clore, G.M.; Gronenborn, A.M.  
submitted to the Brookhaven Protein Data Bank, January 1991  
A:Reference number: A50049; PDB:611B  
A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
R:Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2315-2323, 1991  
A:Title: High-resolution three-dimensional structure of interleukin beta in solution  
A:Reference number: A44675; MUID:91159409  
A:Contents: annotation; (1)H-NMR structural determination  
R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
J. Biol. Chem. 266, 7081-7086, 1991  
A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a  
A:Reference number: A39774; MUID:91201363  
A:Contents: annotation  
R:Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.  
submitted to the Brookhaven Protein Data Bank, December 1989  
A:Reference number: A35016; PDB:1l1B  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269  
R:Finzel, B.C.; Clancy, L.R.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr, B.C.  
J. Mol. Biol. 209, 779-791, 1989  
A:Title: Crystal structure of recombinant human interleukin-beta at 2.0 angstrom res  
A:Reference number: A44666; MUID:90064532  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea  
ved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.  
C:Comment: Interleukin-beta precursor is less heavily myristoylated than interleukin  
C:Genetics:  
A:Gene: IL1B  
A:Cross-references: GDB:120094; OMIM:147720  
A:Map position: 2q13-q21  
A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3  
C:Superfamily: interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop  
F:117-269/Product: interleukin-1 beta #status experimental <IL1>  
F:76/Binding site: myristate (Lys) (covalent) #status experimental  
F:123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 12.8%; Score 104.5; DB 1; Length 269;  
Best Local Similarity 29.6%; Pred. No. 0.0035; Indels 1; Gaps 1;  
Matches 24; Conservative 18; Mismatches 38;

OY 54 KPVIPLGIQGGSLACVETEGPSLOLEDYNIELYKGGSEATRTFFQSSGSAFLKE 113  
I I : I I : : I : I I I I : : : I I I : : : I I : :  
DB 171 KIPVALGLKEKNLYLSCLLLDKDPTQLSDVDPRN-YPKKKMKREKFVNKRINNKLEFE 229  
OY 114 AAAMPWGFELCGPAEPQPVOL 134  
I : I : I : : I I I :  
DB 230 SAQFPNNWIYSTQAENNPVEL 250  
I : I : I : : I I I :

RESULT 14  
JC5646  
A:Title: interleukin-1 beta - horse  
C:Species: Equus caballus (domestic horse)  
C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 20-Jun-2000  
C:Accession: JC5646  
R:Kafo, H.; Yoon, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa,  
Gene 177, 11-16, 1996  
A:Title: Identification of an alternatively spliced transcript of equine interleukin-1  
A:Reference number: JC5646; MUID:97080493  
A:Accession: JC5646  
A:Molecule type: mRNA  
A:Residues: 1-214 <RAT>  
A:CROSS-references: DDBJ:D42165; NID:Q243549; PIDN:BAA22528.1; PID:Q2463550









Db 76 PTLTLEPVNIMELYLCAKESKSTFYRRDMGLTSSFESAAYGNWFLCTVPEADQPVLQTQ 135

Qy 137 ESE-----PSARTKFFFEQ 150

Db 136 LPENGWGNAPITDFYFQ 153

## RESULT 2

US-09-000-630C-23

; Sequence 23, Application US/09000630C

; Patent No. 6018029

; GENERAL INFORMATION:

; APPLICANT: Fuller, Gerald M.

; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor

; TITLE OF INVENTION: Antagonist

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White

; STREET: 2001 Park Place, Suite 1400

; CITY: Birmingham

; STATE: Alabama

; COUNTRY: USA

; ZIP: 35203-2736

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch,

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/000,630C

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/862,730

; FILING DATE:

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 178 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: rat IL-lra sequence

US-09-000-630C-23

Query Match 31.8%; Score 260.5; DB 3; Length 178;

Best Local Similarity 44.5%; Pred. No. 1.1e-23;

Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;

Qy 16 DQKALYTRDGLLVGDPVADNC-CAEKICTLPNRGLDRTKVPFIFGIQGGSRCLACVETE 74

Db 45 NQKTFYLRNQLIAGYLOGPNTKLEEKIDMVP---IDFRNV--FLGIHGKLCCLSCVKS 99

Qy 75 EGPQLQEDVNIIELYKGGEATRTFTFFQSSGSAFRLEAAWPGWFLCGPAEPQPVOL 134

Db 100 DDTKQLQEEVNTIDLNNKEDKRTFTIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy 135 TK-ESEPSARTKFFFEQ 150

Db 160 TNPKEPCVTTKFFOE 176

## RESULT 3

US-08-862-730C-23

; Sequence 23, Application US/08862730C

; Patent No. 6063600

; GENERAL INFORMATION:

; APPLICANT: Fuller, Gerald M.

; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor

; TITLE OF INVENTION: Antagonist

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White

; STREET: 2001 Park Place, Suite 1400

; CITY: Birmingham

; STATE: Alabama

; COUNTRY: USA

; ZIP: 35203-2736

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch,

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/862,730C

; FILING DATE: 5/23/97

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 178 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: rat IL-lra sequence

US-08-862-730C-23

Query Match 31.8%; Score 260.5; DB 3; Length 178;

Best Local Similarity 44.5%; Pred. No. 1.1e-23;

Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;

Qy 16 DQKALYTRDGLLVGDPVADNC-CAEKICTLPNRGLDRTKVPFIFGIQGGSRCLACVETE 74

Db 45 NQKTFYLRNQLIAGYLOGPNTKLEEKIDMVP---IDFRNV--FLGIHGKLCCLSCVKS 99

Qy 75 EGPQLQEDVNIIELYKGGEATRTFTFFQSSGSAFRLEAAWPGWFLCGPAEPQPVOL 134

Db 100 DDTKQLQEEVNTIDLNNKEDKRTFTIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy 135 TK-ESEPSARTKFFFEQ 150

Db 160 TNPKEPCVTTKFFOE 176

## RESULT 4

US-09-417-455-10

; Sequence 10, Application US/09417455

; Patent No. 6294655

; GENERAL INFORMATION:

; APPLICANT: Pace, Ann

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/36328

; CURRENT APPLICATION NUMBER: US/09/417,455

; CURRENT FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: US 09/348,942

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: PCT/US99/04291

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/287,210

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/251,370

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: US 09/229,591

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 09/127,698

; PRIOR FILING DATE: 1998-07-31

; PRIOR APPLICATION NUMBER: US 09/099,818

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 09/082,364

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 09/079,909

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 09/055,010

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 30

;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10  
;; LENGTH: 178  
;; TYPE: PRT  
;; ORGANISM: Rattus norvegicus  
us-09-417-455-10

Query Match 31.8%; Score 260.5; DB 4; Length 178;  
Best Local Similarity 44.5%; Pred. No. 1.1e-23;  
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;  
Qy 16 DQKALYTRDGLLVGDPVADNC-CAEIKCTLPNRLDRTPVIFLGIQGSRLCLACVETE 74  
Db 45 NQKTFYLRNQLIAGYLOGPNKLEKIDMVP---IDFRNV--FLGIHGKGLCLSCVKS 99  
Qy 75 EGPSLQLEDVNIIELYKGGBEATRTFFFOSSGSAFRLEAAWPGWFLCGPAEPQPVOL 134  
Db 100 DDTKLQLEEVNITDLSKNKEEDRRFTFIRSEGTPTTSFSAACPGWFLCTTLEADRPVSL 159  
Qy 135 TK-ESEPSARTKIFYEQ 150  
Db 160 TNTPEEPLIVTKIFYQE 176

RESULT 5  
US-09-417-455-9  
; Sequence 9, Application US/09417455  
; Patent No. 6294655  
; GENERAL INFORMATION:  
; APPLICANT: Ford, Ann  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36328  
; CURRENT APPLICATION NUMBER: US/09/417,455  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: US 09/348,942  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: PCT/US99/04291  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/287,210  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/251,370  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 09/229,591  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 09/127,698  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: US 09/099,818  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: US 09/082,364  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 09/079,909  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/055,010  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-417-455-9

Query Match 31.5%; Score 257.5; DB 4; Length 178;  
Best Local Similarity 44.5%; Pred. No. 2.5e-23;  
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;  
Qy 16 DQKALYTRDGLLVGDPVADNC-CAEIKCTLPNRLDRTPVIFLGIQGSRLCLACVETE 74  
Db 45 NQKTFYLRNQLIAGYLOGPNKLEKIDMVP---IDLHSV--FLGIHGKGLCLSCAKSG 99

Qy 75 EGPSLQLEDVNIIELYKGGBEATRTFFFOSSGSAFRLEAAWPGWFLCGPAEPQPVOL 134  
Db 100 DDTKLQLEEVNITDLSKNKEEDRRFTFIRSEGTPTTSFSAACPGWFLCTTLEADRPVSL 159  
Qy 135 TK-ESEPSARTKIFYEQ 150  
Db 160 TNTPEEPLIVTKIFYQE 176  
RESULT 6  
US-09-000-630C-21  
; Sequence 21, Application US/09000630C  
; Patent No. 6018029  
; GENERAL INFORMATION:  
; APPLICANT: Fuller, Gerald M.  
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor  
; TITLE OF INVENTION: Antagonist  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White  
; STREET: 2001 Park Place, Suite 1400  
; CITY: Birmingham  
; STATE: Alabama  
; COUNTRY: USA  
; ZIP: 35203-2736  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch,  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Microsoft Windows  
; SOFTWARE: WordPerfect 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/000,630C  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/862,730  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: mouse IL-1ra sequence  
US-09-000-630C-21

Query Match 31.2%; Score 255.5; DB 3; Length 178;  
Best Local Similarity 44.5%; Pred. No. 4.4e-23;  
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;  
Qy 16 DQKALYTRDGLLVGDPVADNCCAE-KICTLPNRLDRTPVIFLGIQGSRLCLACVETE 74  
Db 45 NQKTFYLRNQLIAGYLOGPNKLEKIDMVP---IDLHSV--FLGIHGKGLCLSCAKSG 99  
Qy 75 EGPSLQLEDVNIIELYKGGBEATRTFFFOSSGSAFRLEAAWPGWFLCGPAEPQPVOL 134  
Db 100 DDTKLQLEEVNITDLSKNKEEDRRFTFIRSEGTPTTSFSAACPGWFLCTTLEADRPVSL 159  
Qy 135 TK-ESEPSARTKIFYEQ 150  
Db 160 TNTPEEPLIVTKIFYQE 176  
RESULT 7  
US-08-862-730C-21  
; Sequence 21, Application US/08862730C  
; Patent No. 6063600  
; GENERAL INFORMATION:  
; APPLICANT: Fuller, Gerald M.  
; APPLICANT: Fuentes, Nelson L.  
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor  
; TITLE OF INVENTION: Antagonist



Query Match 30.3%; Score 248; DB 3; Length 176;  
Best Local Similarity 39.7%; Pred. No. 3.5e-22;

```

: TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
:
: TITLE OF INVENTION: Antagonist
:
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White
:
: STREET: 2001 Park Place, Suite 1400
:
: CITY: Birmingham
:
: STATE: Alabama
:
: COUNTRY: USA
:
: ZIP: 35203-2736
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Diskette, 3.50 inch,
:
: COMPUTER: IBM compatible
:

```

```

/ SOURCE: PDB FILE: 6.0
/
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER:  US/09/000, 630C
/   FILING DATE:
/   PRIOR APPLICATION DATA:
/     APPLICATION NUMBER:  08/862,730
/     FILING DATE:
/   INFORMATION FOR SEQ ID NO:  22:
/     SEQUENCE CHARACTERISTICS:
/       LENGTH: 177 amino acids
/       TYPE: amino acid
/       STRANDEDNESS: single
/       TOPOLOGY: linear
/     MOLECULE TYPE: rabbit IL-lra sequence
/
/ US-09-000-630C-22

```

```

Query Match      29.5%; Score 241; DB 3; Length 177;
Best Local Similarity 39.2%; Pred. No. 2.5e-21;
Matches 60; Conservative 22; Mismatches 57; Indels 14; Gaps
y      2 CSLPMARYIIKIYADOKALYTRDGLLVGDPVADNC-CAEKICITLPMRGDLRTKVP--IF 58
      | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
b      33 CRMQAFRIWDV---NORTYLRNNQLVAGYLGQPNAKLEERIDVVPLE-----PQLF 82
      | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
y      59 LGIGGSRCLACVETEGPSLOEDVNTIEELYKGEEATRTFFQSSGSASFLEAAAMP 11
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
b      83 LGIORGLCLCSVKYGDKMKLHLEAVNITDLGKNKEQDKRTFIRNSGPTTTFESASCP 14
      | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
y      119 GWFLCGPAEPQPPVQLTKSEPS-ARTKPYFEQ 150
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
143 GWFCTALEADOPVSLNTPDOSIVVTKPYFOE 175
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

US-08-862-730C-22
;
; Sequence 22, Application US/08862730C
; Patent No. 6063600
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M
; APPLICANT: Fuentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400
; CITY: Birmingham
; STATE: Alabama
; COUNTRY: USA

```

```

;
;   MEDIUM TYPE: Diskette, 3.50 inch,
;
;   COMPUTER: IBM compatible
;
;   OPERATING SYSTEM: Microsoft Windows
;
;   SOFTWARE: WordPerfect 6.0
;
;   CURRENT APPLICATION DATA:
;
;   APPLICATION NUMBER: US/08/962,730C
;
;   FILING DATE: 5/23/97
;

```

```

; INFORMATION FOR SEQ ID NO: 22:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 177 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;     MOLECULE TYPE: rabbit IL-1ra
US-08-862-730C-22

```

Query Match	29.5%;	Score	241;	DB	3;	Length	177;
Best Local Similarity	39.2%;	Pred. No.	2.5e-21;				
Matches	60;	Conservative	22;	Mismatches	57;	Indels	14;
Gaps	5;						
QY	2	CSLPMWRYIIKYADOKALYTRDGLLVGPVADNC-CAEIKICTLPNRLDRTKVP--IF	58				
		:   : :     :     :   :   :   :   :   :					
Db	33	CRMQAFRIDWV---NKTTYLRNNOLVAGYLQGPNAKLEERIDVVPL-----POLMF	82				
		:   : :     :     :   :   :   :   :   :					
QY	59	LGIQGGSLCLACVETEETEGPSLOLEDVNIEELYKGGEATRTFFOSSGSAFLEAAAMP	118				
		:   : :     :     :   :   :   :   :   :					
Db	83	LGIQRIGLCISLKVGSKDKMKLHLEAVNTDLGNKKEQDRFTFIIRNSGGTTTFESASCP	142				
		:   : :     :     :   :   :   :   :   :					
	119	GNWFLCGPAEPQQPVQLTKSESPS-ARKTYFEQ	150				
		:   :   :   :   :   :   :   :   :					
Db	143	GNWFLCTALEADQPVSINTPTDDSIIVVKFYFQE	175				
		:   :   :   :   :   :   :   :   :					

Search completed: May 10, 2002, 13:52:52  
Job time: 125 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:50:17 ; Search time 23.86 Seconds  
(without alignments)  
471.883 Million cell updates/sec

Title: US-09-724-583-2  
Perfect score: 818  
Sequence: 1 MCSLPMARYIIRYADQKAL.....QLTKSEPSARTKFVFEQSW 152

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	818	100.0	152	AAE05840	Human FIL-1 theta
2	818	100.0	152	AAE05840	Human interleukin-
3	818	100.0	169	AAE05840	Human interleukin-
4	818	100.0	200	AAE05840	Human interleukin-
5	729.5	89.2	152	AAE05840	Human interleukin-
6	657	80.3	152	AAE05840	Human interleukin-
7	657	80.3	152	AAE05840	Human interleukin-
8	587	71.8	112	AAE05839	Human FIL-1 theta
9	309	37.8	156	AAE05839	Rodent interleukin
10	309	37.8	156	AAE05839	Mouse interleukin
11	309	37.8	156	AAE05839	Murine IL-1 homolo

12	309	37.8	156	21	AAE05840	Murine TANGO-93 pr
13	307	37.5	154	22	AAE05840	Mouse interleukin-
14	307	37.5	155	21	AAE05840	Murine IL-1 recept
15	307	37.5	155	22	AAE05840	Murine IL-1 recept
16	307	37.5	155	22	AAE05840	Murine IL-1 recept
17	307	37.5	155	22	AAE05840	Murine IL-1 recept
18	289	35.3	155	21	AAE05840	Murine interleukin
19	283	34.6	154	22	AAE05840	Human IL-1 homolo
20	283	34.6	155	20	AAE05840	Human interleukin
21	283	34.6	155	21	AAE05840	Human IL-1 recept
22	283	34.6	155	21	AAE05840	Human IL-1 recept
23	283	34.6	155	21	AAE05840	Human IL-1 homolo
24	283	34.6	155	21	AAE05840	Human TANGO-93 pr
25	283	34.6	155	22	AAE05840	Human interleukin-
26	283	34.6	155	22	AAE05840	Human interleukin-
27	283	34.6	155	22	AAE05840	Human IL-1 homolo
28	283	34.6	155	22	AAE05840	Human IL-1 homolo
29	283	34.6	155	22	AAE05840	Human IL-1 homolo
30	283	34.6	155	22	AAE05840	Human IL-1 homolo
31	280	34.2	155	20	AAE05840	Human IL-1 homolo
32	276	33.7	155	21	AAE05840	Human IL-1 homolo
33	276	33.7	155	21	AAE05840	Human IL-1 homolo
34	260.5	31.8	178	20	AAE05840	Human IL-1 homolo
35	260.5	31.8	178	20	AAE05840	Human IL-1 homolo
36	260.5	31.8	178	20	AAE05840	Human IL-1 homolo
37	260	31.8	178	20	AAE05840	Human IL-1 homolo
38	257.5	31.5	178	20	AAE05840	Human IL-1 homolo
39	257.5	31.5	178	20	AAE05840	Human IL-1 homolo
40	248	30.3	151	20	AAE05840	Human IL-1 homolo
41	248	30.3	151	20	AAE05840	Human IL-1 homolo
42	248	30.3	151	20	AAE05840	Human IL-1 homolo
43	241	29.5	177	20	AAE05840	Human IL-1 homolo
44	241	29.5	177	20	AAE05840	Human IL-1 homolo
45	240.5	29.4	159	16	AAE05840	Human IL-1 homolo

ALIGNMENTS

RESULT 1  
AAE05840  
ID AAE05840 standard; Protein; 152 AA.  
XX AC AAE05840;  
XX DT 24-SEP-2001 (first entry)  
XX DE Human FIL-1 theta full-length protein.  
XX KW Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;  
XX KW insulin dependent diabetes mellitus; lymphoma; microbial infection;  
XX KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;  
XX KW tibial muscular dystrophy; inflammation; gene therapy; human.  
XX OS Homo sapiens.  
XX PN WO200155211-A2.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-US02514.  
XX PR 27-JAN-2000; 2000US-0178389.  
XX PA 11-APR-2000; 2000US-0195962.  
XX PI (IMV ) IMMUNEX CORP.  
XX PI Sims JE;  
XX DR WPI; 2001-457718/49.  
XX DR N-PSDB; AAD11148.  
XX PT isolated FIL-1 theta polypeptide to induce or inhibit the induction of

PT fever and to stimulate the immune system for the treatment of microbial  
PT infections -  
XX  
PS Claim 14; Page 5; 65pp; English.  
XX  
CC The invention relates to interleukin-1 (IL-1) family ligand designated  
CC as FIL-1 theta polypeptides and nucleic acid molecules encoding such  
CC polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin  
CC dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/  
CC lymphoma, wrinkle skin syndrome and tibial muscular dystrophy. FIL-1  
CC theta polypeptides are used to activate and/or inhibit the activation  
CC of vascular endothelial cells and lymphocytes; the induction of local  
CC tissue destruction and fever; the stimulation of macrophages and  
CC vascular endothelial cells to produce IL-6 and the induction of  
CC prostaglandins. They are also used to treat inflammation and microbial  
CC infections. FIL-1 theta DNA is useful in antisense therapy and gene  
CC therapy. The present sequence is human FIL-1 theta full-length protein.  
CC  
Sequence 152 AA;

Query Match 100.0%; Score 818; DB 22; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2.4e-86;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCSLPMARYIIKYADOKALYTRDGLLVGDPVADNCCAEKICTLPNRGLDRTKVPFLG 60  
DB 1 mcsllpmariyikyaqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpflg 60  
QY 61 IGGSRCLACVETEPGSLQEDVNIIEELYKGGEATRTFFQSSGSAFRLEAAWPGW 120  
DB 61 iggsrclacveteegpslqledvniieelykggeatrtffqssgsafrleaaawpgw 120  
QY 121 FLCGPAEPQPVQLTKSEPSARTKFFEQSW 152  
DB 121 flcgpaeppqvqltkesepartkfyeqsw 152

RESULT 2  
ID AAB19922 standard; Protein; 152 AA.  
AC AAB19922;  
DT 19-MAR-2001 (first entry)  
XX Human interleukin-1 Hy2 (short version).  
KW Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;  
KW antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;  
KW myeloma; giant cell tumour of bone; acute myelogenous leukaemia;  
KW oral epidermoid carcinoma; squamous cell carcinoma; inflammation;  
KW antitumour; antiinflammatory; diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 44 /note= "polymorphism in nucleotide sequence, alters  
FT Thr-44 to Ile"  
FT  
FT Misc-difference 51 /note= "polymorphism in nucleotide sequence, alters  
FT Asp-51 to Ala"  
FT

XX  
XX WO200071719-A1.  
XX  
XX 30-NOV-2000.  
XX  
XX 22-MAY-2000; 2000WO-US14144.  
XX  
XX 20-MAY-1999; 99US-0316086.  
PR 10-MAR-2000; 2000US-0522964.  
XX  
XX

PA (HYSE-) HYSEQ INC.  
XX Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;  
XX  
XX WPI; 2001-016409/02.  
DR N-PSDB; AAA89175, AAA89176.  
XX  
XX New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,  
PT preventing and treating disorders, such as cancers and inflammatory  
PT diseases -  
XX  
XX Example 5; Page 130-132; 158pp; English.  
XX  
XX The present sequence is that of human interleukin-1 Hy2 (IL-1 Hy2),  
CC a novel member of the interleukin-1 receptor antagonist family.  
CC The sequence is predicted from isolated cDNA clones (see AAA89175 and  
CC AAA89176). Potential polymorphisms in the coding region may alter  
CC the sequence, specifically changing Thr-44 to Ile and Asp-51 to  
CC Ala, which may affect the biological activity of the molecule.  
CC An alternative, extended open reading frame encodes a 200-amino  
CC acid protein (see AAB19924). IL-1 Hy2 polypeptides and polynucleotides  
CC are used to treat cancers involving elevated levels of IL-1, such as  
CC breast adenocarcinoma, brain tumours, melanoma, giant cell tumours  
CC of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or  
CC squamous cell carcinoma, and inflammatory disease mediated by  
CC interleukin-18 (all claimed). They can also be used to diagnose,  
CC prevent or treat shock, thrombosis, acute pancreatitis, arthritis,  
CC vasculitis, lupus, immune complex glomerulonephritis, pancreatic  
CC cell damage, allograft and xenograft transplantation, graft versus  
CC host disease, inflammatory bowel disease, bone degenerative  
CC diseases, diabetes and neurodegenerative disorders.  
XX  
XX Sequence 152 AA;

Query Match 100.0%; Score 818; DB 22; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2.4e-86;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCSLPMARYIIKYADOKALYTRDGLLVGDPVADNCCAEKICTLPNRGLDRTKVPFLG 60  
DB 1 mcsllpmariyikyaqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpflg 60  
QY 61 IGGSRCLACVETEPGSLQEDVNIIEELYKGGEATRTFFQSSGSAFRLEAAWPGW 120  
DB 61 iggsrclacveteegpslqledvniieelykggeatrtffqssgsafrleaaawpgw 120  
QY 121 FLCGPAEPQPVQLTKSEPSARTKFFEQSW 152  
DB 121 flcgpaeppqvqltkesepartkfyeqsw 152

RESULT 3  
AAB19923  
ID AAB19923 standard; Protein; 169 AA.  
XX  
XX AAB19923;  
XX  
XX 19-MAR-2001 (first entry)  
XX  
XX Human interleukin-1 Hy2 (extended form, partial sequence).  
XX  
XX Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;  
KW antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;  
KW myeloma; giant cell tumour of bone; acute myelogenous leukaemia;  
KW oral epidermoid carcinoma; squamous cell carcinoma; inflammation;  
KW antitumour; antiinflammatory; diagnosis; therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO200071719-A1.  
XX  
XX 30-NOV-2000.  
PD

XX PF 22-MAY-2000; 2000WO-US14144.  
XX PR 20-MAY-1999; 99US-0316086.  
XX PR 10-MAR-2000; 2000US-0522964.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;  
XX WPI; 2001-016409/02.  
XX DR N-PSDB; AAA89175.  
XX PT New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,  
XX PT preventing and treating disorders, such as cancers and inflammatory  
XX PT diseases -  
XX PS Example 5; Page 134-145; 158pp; English.  
XX CC The present sequence is that of a human interleukin-1 Hy2 (IL-1 Hy2)  
XX CC non-full length polypeptide, as predicted from an isolated cDNA  
XX CC clone (see AAA89175). A 200-amino acid full-length sequence is given  
XX CC in AAB19924. IL-1 Hy2 is a novel member of the interleukin-1 receptor  
XX CC antagonist family. IL-1 Hy2 polypeptides and polynucleotides are  
XX CC used to treat cancers involving elevated levels of IL-1, such as  
XX CC breast adenocarcinoma, brain tumours, melanoma, giant cell tumours  
XX CC of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or  
XX CC squamous cell carcinoma, and inflammatory disease mediated by  
XX CC interleukin-18 (all claimed). They can also be used to diagnose,  
XX CC prevent or treat shock, thrombosis, acute pancreatitis, arthritis,  
XX CC vasculitis, lupus, immune complex glomerulonephritis, pancreatic  
XX CC cell damage, allograft and xenograft transplantation, graft versus  
XX CC host disease, inflammatory bowel disease, bone degenerative  
XX CC diseases, diabetes and neurodegenerative disorders.  
XX CC Sequence 169 AA;  
SQ

Query Match 100.0%; Score 818; DB 22; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.7e-86;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCSLPMARYIYIKYADOKALYTRDGLLVGDPVADNCCAEKICTLPNGLDRTKVPFLG 60  
Db 18 mcslpmaryyilikyadqkalytrdggllvgdpvadnccaeikictlpnrgldrtkvpflg 77  
OY 61 IQGSRCLACVETEEGPSLQLEDVNIELYKGGEATRTFTFQSSGSAFRLEAAAPGW 120  
Db 78 iqggsrclacveteegpslqledvnieelykggeatrftffqssgsafrleaaapgw 137  
121 FLCGPAEPQPVOLTKESPSARTKFFEQSW 152  
Db 138 flcgpaeppqvptkeseptsartkffyfeqsw 169

RESULT 4  
AAB19924  
ID AAB19924 standard; Protein; 200 AA.  
XX AC AAB19924;  
XX DT 19-MAR-2001 (first entry)  
XX DE Human interleukin-1 Hy2 (long version).  
XX KW Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;  
XX KW antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;  
XX KW myeloma; giant cell tumour of bone; acute myelogenous leukaemia;  
XX KW oral epidermoid carcinoma; squamous cell carcinoma; inflammation;  
XX KW antitumour; antiinflammatory; diagnosis; therapy.  
OS Homo sapiens.  
XX

PN WO200071719-AL.  
XX PD 30-NOV-2000.  
XX PF 22-MAY-2000; 2000WO-US14144.  
XX PR 20-MAY-1999; 99US-0316086.  
XX PR 10-MAR-2000; 2000US-0522964.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;  
XX WPI; 2001-016409/02.  
XX DR N-PSDB; AAA89177, AAA89178.  
XX PT New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,  
XX PT preventing and treating disorders, such as cancers and inflammatory  
XX PT diseases -  
XX PS Example 5; Page 144-145; 158pp; English.  
XX CC The present sequence is that of human interleukin-1 Hy2 (IL-1 Hy2),  
XX CC a novel member of the interleukin-1 receptor antagonist family.  
XX CC The sequence is predicted from the genomic DNA sequence (see  
XX CC AAA89177) and a predicted cDNA sequence (see AAA89178). An alternative  
XX CC open reading frame (see AAA89176) encodes a 152 polypeptide (see  
XX CC AAB19922). IL-1 Hy2 polypeptides and polynucleotides are used to  
XX CC treat cancers involving elevated levels of IL-1, such as  
XX CC breast adenocarcinoma, brain tumours, melanoma, giant cell tumours  
XX CC of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or  
XX CC squamous cell carcinoma, and inflammatory disease mediated by  
XX CC interleukin-18 (all claimed). They can also be used to diagnose,  
XX CC prevent or treat shock, thrombosis, acute pancreatitis, arthritis,  
XX CC vasculitis, lupus, immune complex glomerulonephritis, pancreatic  
XX CC cell damage, allograft and xenograft transplantation, graft versus  
XX CC host disease, inflammatory bowel disease, bone degenerative  
XX CC diseases, diabetes and neurodegenerative disorders.  
XX CC Sequence 200 AA;  
SQ

Query Match 100.0%; Score 818; DB 22; Length 200;  
Best Local Similarity 100.0%; Pred. No. 3.4e-86;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCSLPMARYIYIKYADOKALYTRDGLLVGDPVADNCCAEKICTLPNGLDRTKVPFLG 60  
Db 49 mcslpmaryyilikyadqkalytrdggllvgdpvadnccaeikictlpnrgldrtkvpflg 108  
OY 61 IQGSRCLACVETEEGPSLQLEDVNIELYKGGEATRTFTFQSSGSAFRLEAAAPGW 120  
Db 109 iqggsrclacveteegpslqledvnieelykggeatrftffqssgsafrleaaapgw 168  
121 FLCGPAEPQPVOLTKESPSARTKFFEQSW 152  
Db 169 flcgpaeppqvptkeseptsartkffyfeqsw 200

RESULT 5  
AAB84999  
ID AAB84999 standard; Protein; 154 AA.  
XX AC AAB84999;  
XX DT 06-AUG-2001 (first entry)  
XX DE Human interleukin-1 receptor antagonist (NOVINTRA A) polypeptide.  
XX KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
XX KW gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;  
XX KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;  
XX KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;

KW antiasthmatic; antiallergic.  
XX Homo sapiens.  
OS WO200140291-A2.  
PN 07-JUN-2001.  
XX  
PD  
XX  
PF 06-DEC-2000; 2000WO-US33029.  
XX  
PR 06-DEC-1999; 99US-0169056.  
XX  
PR 09-DEC-1999; 99US-0169866.  
XX  
PR 09-DEC-1999; 99US-0169886.  
XX  
PR 10-DEC-1999; 99US-0170252.  
XX  
PR 12-JAN-2000; 2000US-0175740.  
XX  
PR 05-DEC-2000; 2000US-0170252.  
XX  
(CURA-) CURAGEN CORP.

PI Burgess CE, Prayaga SK, Shinkels RA, Rastelli L, Zerhusen BD;  
XX Mezes PS;  
DR WPI; 2001-374790/39.  
DR N-PSDB; AAF83868.  
XX  
XX Novel isolated human transmembrane, neuromedin peptide  
PT gonadotropin-like protein and interleukin-1 receptor antagonist  
PT proteins, useful for treating cancer, immune response disorder,  
PT metabolic function disorders -  
XX  
PS Claim 1; Fig 9B; 138pp; English.

XX The invention provides novel polypeptides (NOVX) selected from human  
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
CC antagonist proteins (NOVINTRA A and B). The invention also provides  
CC methods in which a NOVX polypeptide, polynucleotide and antibody are  
CC used in the detection, prevention and treatment of a broad range of  
CC pathological states. NOVTRAN can be used to treat a cell signaling  
CC disorder such as cancer, immune response disorder, hematopoietic  
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
CC central nervous system, breast, colon, ovary, kidney, prostate and  
CC thyroid. NOVGON can be used to treat reproductive development disorder,  
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used  
CC to treat bone metabolism or structure disorder, inflammatory response  
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
CC arthritis and cancer. The present sequence represents the NOVINTRA A  
CC polypeptide.

XX Sequence 154 AA;

Query Match 89.2%; Score 729 5; DB 22; Length 154;  
Best Local Similarity 93.9%; Pred. No. 3.8e-76;  
Matches 139; Conservative 0; Mismatches 2; Indels 7; Gaps 1;  
QY 12 IKYADQKALYTRDQQLLVGDPVADNCCAEKICTLPNRGLDRTKVPFLGIGGSRCLACY 71  
DB 7 Ikyadqkalytrdgqllvgdpvadnccaekicilpnrglartkvipflgiggsrclacy 66  
QY 72 ETEEGPSLQLE-----DVNTEELYKGEEATRTFTFQSSSGSAFRLAAAPGWFLCG 124  
DB 67 eteegpslqlpstlppqdvnieelykggeeatrtftfqqssgsafrleaaawpwyfclg 126  
QY 125 PAEPQPPVQLTKSEPSARTKFFQSW 152  
DB 127 paepqpqvltkeseptsartkfyeqsw 154

RESULT 6  
AAE05841  
ID AAE05841 standard; Protein; 152 AA.

XX AAE05841;  
AC 24-SEP-2001 (first entry)  
DT XX  
XX Mouse FIL-1 theta protein.  
DE  
XX  
XX Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;  
KW insulin dependent diabetes mellitus; lymphoma; microbial infection;  
KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;  
KW tibial muscular dystrophy; inflammation; gene therapy; mouse.  
XX  
OS Mus musculus.  
XX WO20015211-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02514.  
XX  
XX 27-JAN-2000; 2000US-0178389.  
PR 11-APR-2000; 2000US-0195962.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Silms JE;  
XX WPI; 2001-457718/49.  
DR N-PSDB; AAD11158.  
XX  
XX Isolated FIL-1 theta polypeptide to induce or inhibit the induction of  
PT fever and to stimulate the immune system for the treatment of microbial  
PT infections -  
XX  
XX Claim 17; Page 6; 65pp; English.

XX The invention relates to interleukin-1 (IL-1) family ligand designated  
CC as FIL-1 theta polypeptides and nucleic acid molecules encoding such  
CC polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin  
CC dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/  
CC lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1  
CC theta polypeptides are used to activate and/or inhibit the activation  
CC of vascular endothelial cells and lymphocytes; the induction of local  
CC tissue destruction and fever; the stimulation of macrophages and  
CC vascular endothelial cells to produce IL-6 and the induction of  
CC prostaglandins. They are also used to treat inflammation and microbial  
CC infections. FIL-1 theta DNA is useful in antisense therapy and gene  
CC therapy. The present sequence is mouse FIL-1 theta protein.

XX Sequence 152 AA;

Query Match 80.3%; Score 657; DB 22; Length 152;  
Best Local Similarity 82.1%; Pred. No. 8.5e-68;  
Matches 124; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
QY 1 MCSLPMARYIYIKVADOKALYTRDQQLLVGDPVADNCCAEKICTLPNRGLDRTKVPFLG 60  
DB 1 mcsllpmariyikdahgkalytrngqlllgdpdsdnyspekvcilpnrgldrskvpflg 60  
QY 61 IQGGSRLACVTEEGPSLQLEDVNTEELYKGEEATRTFTFQSSSGSAFRLAAAPGW 120  
DB 61 -maggscclacvktregplqlgdnviedlykggeatrtftfqlsgsafrleaaacpgw 120  
QY 121 FLCGPAEPQPPVQLTKSEPSARTKFFQSW 151  
DB 121 flcgpaepqpqvltkeseptsthtefyems 151

RESULT 7  
AAE05841  
ID AAE05841 standard; Protein; 152 AA.  
XX



XX Interleukin; IL-1 delta: polyclonal antibody; IL-1 epsilon; cytokine;  
 KW inflammatory response; immune system; diagnosis; agonist; antagonist;  
 KW chemokine.  
 XX  
 OS Mus sp.  
 XX  
 PN W09847921-A1.  
 XX  
 PD 29-OCT-1998.  
 XX  
 PF 17-APR-1998; 98WO-US06879.  
 XX  
 PR 06-AUG-1997; 97US-0051111.  
 PR 21-APR-1997; 97US-0837627.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 Bazan JF, Hedrick JA, Kastelein RA, Sana TR;  
 WPI; 1998-609976/51.  
 DR N-PSDB; AAV71958.  
 XX  
 PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.  
 PT regulating the immune system and inflammatory responses  
 XX  
 PS Claim 1; Pages 89-90; 113pp; English.  
 XX  
 CC This represents a rodent interleukin (IL)-1 delta polypeptide. The  
 CC invention relates to a recombinant polypeptide that specifically binds  
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid  
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these  
 CC IL polypeptides are used to regulate a cell involved in an inflammatory  
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are  
 CC used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and  
 CC the corresponding nucleic acids regulate development and/or the immune  
 CC system, and can be used to diagnose and treat conditions associated with  
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1  
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,  
 CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1  
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion  
 CC protein with another cytokine or chemokine.  
 XX  
 SQ Sequence 156 AA;  
 Query Match 37.8%; Score 309; DB 19; Length 156;  
 Best Local Similarity 45.2%; Pred. No. 1.1e-27;  
 Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;  
 QY 1 MCSLPMARYIIVADOKALYTRDGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFL 59  
 Db 1 mmvlsqalcfrmkdsalkvlylhnnqllagglaekvikgeelsvvpnralspsvll 60  
 QY 60 GIGGSRCLACVETEGPSLOLEDVNIIELYKGGEEATRTFFQSSGSAFLEAAWPG 119  
 Db 61 gvdggsqclsc-gtekgpiklepvnimelylgakesksftfrrdmgltssesaaypg 119  
 QY 120 WFLCSPABPQOPVOLTKESPSA----RTKFFFEQ 150  
 Db 120 wfictspadpvriltqipedawdaptidfyfqq 154  
 RESULT 10  
 AAY28407  
 ID AAY28407 standard; Protein: 156 AA.  
 XX  
 AC AAY28407;  
 XX  
 DT 28-SEP-1999 (first entry)  
 XX  
 DE Mouse interleukin 1 delta.  
 XX

KW Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;  
 KW insulin-dependent diabetes mellitus; wrinkly skin syndrome;  
 KW T-cell leukemia; lymphoma; tibial muscular dystrophy.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09935268-A1.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 08-JAN-1999; 99WO-US00514.  
 XX  
 PR 01-JUN-1998; 98US-0087393.  
 PR 09-JAN-1998; 98US-0071074.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 XX Sims JE;  
 XX  
 WPI; 1999-458310/38.  
 DR N-PSDB; AAX89431.  
 XX  
 PT Murine and Human interleukin 1 delta DNA, polypeptides and its  
 PT fragments, useful as molecular weight markers  
 XX  
 PS Claim 1; Page 67; 72pp; English.  
 XX  
 CC The present sequence represents mouse interleukin 1 delta (IL-1 delta).  
 CC IL-1 delta proteins are useful for the determination of the molecular  
 CC weight of a sample protein. The protein and its fragments are useful as  
 CC controls for peptide fragmentation. This is useful for determining the  
 CC isoelectric point of a sample protein. Antibodies generated against  
 CC IL-1 delta and its fragmented peptides can be used to enhance the  
 CC accuracy of these molecular weight markers to determine the apparent  
 CC molecular eight and isoelectric point of a sample protein. IL-1 delta  
 CC can be used to screen for potential inhibitors of activity associated  
 CC with IL-1 delta counter-structure molecules. IL-1 delta can also be used  
 CC as therapeutic agents for the treatment of diseases mediated by IL-1  
 CC delta. IL-1 delta may be used as a reagent in studying the interleukin 1  
 CC (IL-1) signalling pathway, or as a reagent to block IL-1 signalling. The  
 CC IL-1 delta coding sequences can be used to identify human chromosome 2,  
 CC and to identify genes associated with certain diseases, especially with  
 CC region 2q11-12, including glaucoma, ectodermal dysplasia, insulin-  
 CC dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukemia/  
 CC lymphoma and tibial muscular dystrophy.  
 XX  
 SQ Sequence 156 AA;

Query Match 37.8%; Score 309; DB 20; Length 156;  
 Best Local Similarity 45.2%; Pred. No. 1.1e-27;  
 Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;  
 QY 1 MCSLPMARYIIVADOKALYTRDGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFL 59  
 Db 1 mmvlsqalcfrmkdsalkvlylhnnqllagglaekvikgeelsvvpnralspsvll 60  
 QY 60 GIGGSRCLACVETEGPSLOLEDVNIIELYKGGEEATRTFFQSSGSAFLEAAWPG 119  
 Db 61 gvdggsqclsc-gtekgpiklepvnimelylgakesksftfrrdmgltssesaaypg 119  
 QY 120 WFLCSPABPQOPVOLTKESPSA----RTKFFFEQ 150  
 Db 120 wfictspadpvriltqipedawdaptidfyfqq 154

RESULT 11  
 AAY92260  
 ID AAY92260 standard; Protein: 156 AA.  
 XX  
 AC AAY92260;  
 XX  
 DT 10-AUG-2000 (first entry)

DE XX Murine IL-1 homologue, zilla3.

DE XX Generic; interleukin-1; IL-1; homologue; zilla3; anti-inflammatory;

XX KW antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;

XX KW antirheumatic; osteopathic; antipsoriatic; antibacterial; cytostatic;

XX KW immunosuppressive; antiulcer; antidiabetic; nephrotropic; vasotropic;

XX KW vulnerary; 2q14.

OS XX Mus musculus.

PN XX WO200020595-A1.

XX XX 13-APR-2000.

XX XX 08-OCT-1999; 99WO-US23533.

XX XX 08-OCT-1998; 98US-0169745.

XX XX (ZYMO ) ZYMOGENETICS INC.

PA XX Sheppard PO, West RR, Clegg CH;

XX N-PSDB; AAA09198.

DR WPI; 2000-303780/26.

XX N-PSDB; AAA09198.

XX Proteins useful for treatment of inflammatory conditions such as

PT rheumatoid arthritis and psoriasis are agonists or antagonists forms of

PT new interleukin-1 homologue

XX Example 7; Page 59-60; 64pp; English.

XX This shows an interleukin-1 (IL-1) homologue, designated zilla3. A 350

CC bp probe generated from the DNA sequence by PCR using AAA09199-200 was

CC used to analyze human northern blots.

CC It is believed that zilla3 acts through IL-1 receptors. In general,

CC zilla3 proteins having a Lys residue at position 148 will have

CC anti-inflammatory activity (e.g. AA92256), whilst those having Asp

CC (see AA92254) or Glu at this position will have pro-inflammatory

CC action. Zilla3 is used to modulate an immune response in an animal

CC (claimed). Antagonists zilla3 forms may be used to treat or prevent

CC chronic inflammatory diseases such as rheumatoid arthritis,

CC osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage

CC after ischemia, to treat septic shock, graft-versus-host disease and

CC leukemia. The antagonists may also alleviate inflammatory bowel disease

CC including Crohn's disease and ulcerative colitis, insulin-dependent

CC diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral

CC ischemia. Agonist forms of zilla3 may promote wound healing by IL-1

CC effects on growth factor secretion and cell proliferation. They may also

CC treat infections, especially gastrointestinal infections.

Sequence 156 AA;

Query Match 37.8%; Score 309; DB 21; Length 156;

Best Local Similarity 45.2%; Pred. No. 1.1e-27;

Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;

QY 1 MCSLPMARYIYIKYADQKALYTRDGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFL 59

Db 1 mmvlsqalcfrmkdsalkvlyhnnqllagglhaekvikgeelsvvpnrldaspsvil 60

QY 60 GIOGSRCLACVETEGPSLQLEDVNIIELYKGGEATRTFFQSSGSAFRLEAAWPG 119

Db 61 gvqgsgqlsc-gtekqplkplevnmelylgakeskftfyrrdmgtltsfesaaypg 119

QY 120 WFLCGPAPQPPQVOLTKESEPSA---RTKEYFEQ 150

Db 120 wflctspadqpvrlltqipedpawdapitdtyfdq 154

RESULT 12

AA45061

ID XX AAY45061 standard; Protein; 156 AA.

AC XX AAY45061;

DT 31-MAY-2000 (first entry)

XX Murine TANGO-93 protein.

DE XX

XX TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;

KW Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;

KW immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; asthma;

KW antiinflammatory; antibacterial; antiulcer; cytostatic; immunomodulator;

KW osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;

KW graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;

KW septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia;

KW liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;

KW autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;

XX systemic lupus erythematosus; forensic; transgenic animal.

OS Mus sp.

XX WO200008045-A2.

XX 17-FEB-2000.

XX 06-AUG-1999; 99WO-US17886.

XX 07-AUG-1998; 98US-0131263.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y;

XX WPI; 2000-205669/18.

DR N-PSDB; AAZ50811.

XX Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful

PT for treating a variety of cellular processes e.g. asthma, rheumatoid

PT arthritis, psoriasis and autoimmune diseases

XX Claim 9; Fig 1; 113pp; English.

XX The present sequence is the murine TANGO-93, a secreted protein, that

CC belongs to the cytokine superfamily. It plays a role similar to secreted

CC Interleukin-1 receptor antagonist (IL-1ra) and its expression is

CC developmentally regulated in liver, heart and bone marrow. TANGO-93

CC modulates immune mediated inflammation and IL-1 gene or protein

CC expression. TANGO-93 is useful as a modulating agent for regulating

CC cellular processes like asthma, graft vs-host disease, rheumatoid

CC arthritis, psoriasis, inflammatory bowel disease, septic shock,

CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,

CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,

CC cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune

CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences

CC are useful in forensic biology, for diagnostic and prognostic assays,

CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA

CC sequences are useful as hybridisation probes and primers, for isolation

CC of TANGO-93 sequence and for the creation of transgenic animals.

XX Sequence 156 AA;

QY 1 MCSLPMARYIYIKYADQKALYTRDGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFL 59

Db 1 mmvlsqalcfrmkdsalkvlyhnnqllagglhaekvikgeelsvvpnrldaspsvil 60

QY 60 GIOGSRCLACVETEGPSLQLEDVNIIELYKGGEATRTFFQSSGSAFRLEAAWPG 119

Db 61 gvqgsgqlsc-gtekqplkplevnmelylgakeskftfyrrdmgtltsfesaaypg 119

Query Match 37.8%; Score 309; DB 21; Length 156;

Best Local Similarity 45.2%; Pred. No. 1.1e-27;

Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;

Query Match 37.58; Score 307; DB 21; Length 155;

Query Match 37.58; Score 307; DB 21; Length 155;



Best Local Similarity 47.8%; Pred. No. 1.9e-27;  
Matches 66; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

	QY	18	KALYTRGQLLVGDVPADNCC-AKICTLPNRGLDRTKVPTFLIGGGSRCLACVETEFG76
	Dd	17	kviylhnqlladglhaekvikgeisvvpnrldalslpvilgvgggsgqlsc-gtek975
	QY	77	PSLQEDVNTEELYKGGEATRFTFFOSSGSFAFLAAAWPGWFLCGPAEPOQPVLTK136
	Dd	76	pilklepvnimelygakeskstffryrdmgtltsfesaaypgvfictspedagpvritq135
	QY	137	ESEPSA----RKTFEFQE150
	Dd	136	ipedpawdapitdfyfqq153

Search completed: May 10, 2002, 13:52:33  
Job time: 136 sec

RESULT 15  
AAB35261  
ID AAB35261 standard; Protein; 155 AA.  
XX  
AC AAB35261;

08-MAY-2001 (first entry)  
DE Murine IL-IL1.

Mouse; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
 KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
 KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
 KW osteoporosis; systemic lupus erythematosus.

OS Mus sp.

WO200105974-A2

XX  
PD  
25-JAN-2001.

17-JUL-2000: 2000WO-US19508.

PR 16-JUL-1999: 99US-0144298

XX PA (INTE-) INTERLEUKIN GENETICS INC.

PI Nicklin M, Barton J:

AA  
DR WPI: 2001-091974/10.

AA PT PT

Claim 11: Fig 3: 150pp: English.

The present invention provides the protein and coding sequences of the human and murine Interleukin-11 (IL-11) proteins. The IL-11 gene is located between the IL-1beta and IL-1 receptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis, severe periodontal disease and pregnancy complications. The present sequence is the murine IL-11 protein.

AA	Sequence	155 AA;
SQ		

Query Match 37.58; Score 307; DB 22; Length 155;

Matches 66: Conservative 20: Mismatches 46  
BEST LOCAL SIMILARITY 47.8%; Pred. No. 1.9e-27;

QY 18 KALYTRDQQLVGDVPADNCC-AEICTLTPNRGLDRTPVFIQGGSRCLACVETEEG 76

Db 17 kvlylhnnql laqqlhaekvikqeelsvvpnr aldaslspvllavagqsgclsc-ateka 75

Qy 77 PSLQLEDVNIIEELYKGGEATRTFTFQSSSGSAFRLEAAAMPGWFLCGPAEPQPQLTK 136  
Db 76 pilklepvnimelylqakesktsftfyrdmgltsfesaaypgwflctsheadqpvrltq 135



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 04:46:47 ; Search time 2153.14 Seconds  
(without alignments)  
6393.869 Million cell updates/sec

Title: US-09-724-583-1

Perfect score: 1020

Sequence: 1 caggatcagggtccagga.....acctctaaaaaaaaaaaaa 1020

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmd:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pin:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	714.8	70.1	900	11 AY026753	AY026753 Homo Sapi
c	250.2	24.5	285	10 BI051175	BI051175 CM2-GN028
c	244.2	23.9	589	12 AQ0766579	AQ0766579 HS_2192.B
c	168.6	16.5	574	9 BE067002	BE067002 PMO-BT034
c	137.2	13.5	507	9 AI889529	AI889529 wh05q02.x
c	128	12.5	459	9 AI393136	AI393136 tg41c11.x
c	127.4	12.5	392	9 AA417044	AA417044 zol13402.s
c	126.2	12.4	718	12 AQ0780593	AQ0780593 HS_3138.A
c	125	12.3	612	12 AQ356956	AQ356956 CITBI-EI-
10	122.2	12.0	533	12 AQ442721	AQ442721 HS_5116.B
11	121	11.9	526	12 AQ318555	AQ318555 RPC111-90
c	116.6	11.4	375	9 AA447609	AA447609 zw82406.s
c	115.8	11.4	670	12 AG087298	AG087298 Pan trogl
c	115.4	11.3	634	12 B54722	B54722 CIT-Hsp-384
c	114.6	11.2	525	12 AQ405885	AQ405885 HS_5043.B
c	114.6	10.9	439	12 AQ112190	AQ112190 CIT-HSP-2
15	111.6	10.9	1051	11 AK009741	AK009741 Mus muscu
17	111.6	10.9	1051	11 AK009741	AK009741 Mus muscu

18	111.6	10.9	1199	11 AK008977	AK008977 Mus muscu
19	110.8	10.9	726	10 BI089828	BI089828 602855071
20	110.8	10.9	858	10 BI090567	BI090567 602855674
21	110.8	10.9	932	9 AL545100	AL545100 AL545100
22	109.8	10.8	539	12 AQ418783	AQ418783 RPC1-11-2
23	109.2	10.7	603	10 BF793888	BF793888 602255284
c	108.2	10.6	668	12 AQ626032	AQ626032 CITBI-EI-
c	107.2	10.5	430	9 AA194145	AA194145 zr37904.s
c	106.6	10.5	702	12 AQ627034	AQ627034 CITBI-EI-
c	106.6	10.5	705	12 AQ624891	AQ624891 CITBI-EI-
c	106	10.4	349	9 AW592873	AW592873 hg04401.x
c	106	10.4	441	10 H63593	H63593 yr36c04.r1
c	104.4	10.2	2843	11 AK014576	AK014576 Mus muscu
c	104.2	10.2	607	12 BH316806	BH316806 CH230-194
32	104	10.2	423	12 AQ491155	AQ491155 RPC1-11-2
33	103.6	10.2	584	12 AQ386543	AQ386543 RPC111-15
34	103.6	10.2	710	12 AQ351848	AQ351848 CITBI-EI-
35	103.2	10.1	570	9 AW954120	AW954120 EST366190
36	102.8	10.1	530	12 AQ462403	AQ462403 HS_5130.A
c	101.6	10.0	623	9 AW894443	AW894443 CM2-NN003
c	100.8	9.9	507	12 AQ537983	AQ537983 RPC1-11-3
c	100.2	9.8	594	10 BI961215	BI961215 MON01-7.E
c	99.8	9.8	460	10 BF766876	BF766876 PM2-CS002
c	99.8	9.8	487	9 AUI55269	AUI55269 AUI55269
c	99.8	9.8	583	12 AQ263967	AQ263967 CITBI-EI-
c	99.6	9.8	447	9 AA194142	AA194142 zr37903.r
c	99.6	9.8	467	12 AQ062337	AQ062337 CIT-HSP-2
45	99.6	9.8	651	12 AG151628	AG151628 Pan trogl

#### ALIGNMENTS

RESULT 1	AY026753	AY026753	900 bp	mRNA	linear	HTC 13-JUL-2001
LOCUS	Homo sapiens interleukin-1 receptor antagonist FKSG75	mRNA, complete cds.				
DEFINITION	AY026753	HTC.				
ACCESSION	AY026753.1	GI:12829965				
VERSION						
KEYWORDS	human.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	Wang,Y.-g., Li,T. and Gong,L.					
AUTHORS	Identification and characterization of FKSG75, a novel member of the interleukin-1 family					
TITLE	Unpublished					
JOURNAL	2 (bases 1 to 900)					
REFERENCE	Wang,Y.-g.					
AUTHORS	Direct Submission					
TITLE	Submitted (01-FEB-2001) Beijing FENGKESHENG Function Gene Technology Ltd., 4 You Tiao Lu Chang Street, Xuanwu District, Beijing 100050, P.R.China					
JOURNAL	Location/Qualifiers					
FEATURES	1..900					
source	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/chromosome="2"					
	/map="2p14"					
gene	1..900					
	/gene="FKSG75"					
CDS	91..525					
	/gene="FKSG75"					
	/notes="similar to IL1RN and IL1H1"					
	/codon_start=1					
	/product="interleukin-1 receptor antagonist FKSG75"					
	/protein_id="AAK01948.1"					
	/db_xref="GI:12829966"					
	/translation="MSSSFUPELPKSLQHGVPISLSSILEKICILNRIAR TKVPIPLGQSGSLACVETEGPSLQLEDVNIIEELKKGEEATRTTFQSSGSASF					



ORGANISM	Homo sapiens									
REFERENCE	Eumkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 (bases 1 to 589) Mahairas,G.G., Wallace Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.									
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome									
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)									
MEDLINE	99380589									
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2192 row: J column: 17 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 589.									
FEATURES	Location/Qualifiers 1..589 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_plate="2192 Col=17 Row=J" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"									
BASE COUNT	152 a	147 c	100 g	135 t	55 others					
ORIGIN										
Query Match	23.9%; Score 244.2; DB 12; Length 589;									
Best Local Similarity	87.3%; Pred. No. 5.3e-50;									
Matches 267;	Conservative	0;	Mismatches	39;	Indels	0;	Gaps	0;		
QY	703	aatgagagacaatcctgggtatcctctgtgggtcagtttaataacaaagaggaagcag	762							
Db	586	ATCAGAGAGACTATCGGGTAATCTTTGTGGGCTCAGTTTAATCAACAAGTCAGGCAG	527							
QY	763	gaagggagatcgagagagaatggaagataccatgcttctaatttgaagatggagtga	822							
Db	526	GAAGGGAGATCAGACAGAGAATCAAGATGCCATGATTCTAATTTGAAGATGGAGGA	467							
QY	823	gggccttgagccaacaatcaggtgtttttagaagtgtaaagccaaggaacgaat	882							
Db	466	GGGCGATTACTCACCAGTCAGGTGTTTGAAGGTGAAGCAAGTCAGTCGGAT	407							
QY	883	tctctctagtgctccggaaggacaacagctcttgacacatggaatttcagctcagtgac	942							
Db	406	TCTCTTCTAGAGTCTCTGGAAGGAACTCAGCTCTTGACACATGGATTTCGGCTCAGTGAC	347							
QY	943	accatttcagactctcagctccacaactataataataaactgtttattgttaaac	1002							
Db	346	NCCATTTCGTATTTTTCACCTCCACGAATATAGATAATGANTTTGTGTATTGTGTACCC	287							
QY	1003	ctctaa	1008							
Db	286	ATCTAA	281							
RESULT	4									
LOCUS	BE067002									
DEFINITION	PM0-BF0340-170100-004-b01 BF0340 Homo sapiens cDNA, mRNA sequence.									
ACCESSION	BE067002									
VERSION	BE067002.1									
KEYWORDS	EST.									



```
Db 358 TTTTCATCCCTGGAACTCTGAATACATTTCTTTATGTGGCAAAAGGACTTTTGGCGTGT 299
QY 683 gattatgttaagatcttgaatgaggagacaatcctcgttatactcttggtggtcagttg 742
Db 298 GATTAAACTTAAAGCACTTGAAATAGGAGATTCTCCGGGATCGTCAGATGCATCAATG 239
QY 743 taatcacagaagagagcaggagagagagagagagagagagagagagagagagagagagag 802
Db 238 TAACAAGNAG-----CAGTCAGAGTCAGGCTGGAAGCGCGTATGCTGC 196
QY 803 taatttgaagatgagagtgaggggcttgagccacaataatgcaggtgtttttagaaggtg 862
Db 195 TGGCTTTTGAAGGCGAGATGAAGGGG-----CAAGGAAATTAGGGTGGTCTCTAGAACTG 142
QY 863 gaaagccaaaggaacgagattctctctagagagtcctcgggaaggaacacagc--tcttgac 920
Db 141 GAAAAGCAANTGAATTTGATTCTCCCTTAGAGCTTTCAGAAGGAATGACAGCCTTGCCAC 82
QY 921 acatgagatcagtcagtcagccacttctcagacttctcagacttctcagacttctcagactt 980
81 ACCCTTCATTTTAGACAGTGAACACTGATTTTGTAGACTTCTGACTGCCAGAACTGTAAGATA 22
QY 981 ataaactgtgttattgttaa 1001
Db 21 ATAAATGATATTCATTGAA 1

RESULT 7
AA417044/c AA417044 mRNA linear EST 09-NOV-1997
LOCUS zulf3d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731715
3', mRNA sequence.
ACCESSION AA417044
VERSION AA417044
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 392)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubucque, T., Geisel, G., Jost, S.,
Kriznan, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, J., Wyllie, J., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Contact: Wilton RK
Unpublished (1997)
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 715 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 254.
FEATURES
Source 1..392
/organism="Homo sapiens"
/db_xref="GDB:5928790"
/db_xref="taxon:9606"
/clone="IMAGE:731715"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATGATGAAGTGGAGCGCGCCCAATTTTGTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
```

```
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pMT3D vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 96 a 99 c 66 g 131 t
ORIGIN
Query Match 12.5% Score 127.4; DB 9; Length 392;
Best Local Similarity 65.0% Pred. No. 4.6e-21;
Matches 258; Conservative 0; Mismatches 121; Indels 18; Gaps 4;
QY 617 tcacatcctaataccc-aagatctgtgcataatgttaccatacatgtccaaagaggtttg 675
Db 392 TCCACATCCTAATCTCCCTGGGACCTATGAATATGTTACCTTACATGGTAAAAAGGATTTTG 333
QY 676 caaatgtattatgtaaggtcttgaatgaggagacaatcctcgttatactcttggtggtg 735
Db 332 CAGATGTGACTAAATGAAGACTCTTGATATGAGGAGATTACCTTGGATTATCCATGTGGA 273
QY 736 ctc-----agtttaatcacagaagagggcaggagagagagagagagagagagagagag 791
Db 272 CCCGAGGATATCTATGAGGGAAGAGGGGATGTCAGAGAGATCAGATCGGAAAAAGGAATG 213
QY 792 taccatgcttctaatttgaagatggagtgagg-----ggccttgagccaacaaatcgag 846
Db 212 TTCAAGAAAGCAGAGGTGACAGATGATGTGAAGATCCTGGCTTTGAAGATGGACTGCAAG 153
QY 847 gtgtttttagaagggtggaagccaaagcaggagattctctctctagatgtcccggaagga 906
Db 152 TGGTTTGTAAAAACCTGGAAGGGCAAGAAATTAATTTCTCCCTTGAACCTTGCAGAAAGAA 93
QY 907 acacagctctgacacatggtttcagctcagtcagtcagccacttctcagacttctgacctcc 966
Db 92 ACACAGACCTTGAC-----TTTAGCCCAAGTAAGACCCATTTGGGACCTCTGACCTCC 41
QY 967 acaactataataataaactgtgttattgttaaac 1003
Db 40 AGAACTGTAAAGATAATAAATAGTGTGTTTAAAGCC 4
RESULT 8
AQ780593/c AQ780593 718 bp DNA linear GSS 02-AUG-1999
LOCUS HS-3138.AL_B02.T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-3138 Col-3 Row-C, DNA sequence.
ACCESSION AQ780593
VERSION AQ780593.1 GI:5683553
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3138 row: C column: 3
Seq primer: T7
Class: BAC ends
```





scanning the human genome  
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 99380589  
 Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.htsc.washington.edu  
 Plate: 692 row: N column: 8  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 533.

# FEATURES

Source  
 1..533  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate:692 Col=8 Row=N"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACE3.6 vector at EcoRI sites"  
 178 a 98 c 115 g 135 t 7 others

Query Match 12.0%; Score 122.2; DB 12; Length 533;  
 Best Local Similarity 64.4%; Pred. No. 9.3e-20;  
 Matches 269; Conservative 0; Mismatches 129; Indels 20; Gaps 5;  
 Db 561 ccaagctcctcgtcagggctctgtgtagcagaataatgtcccccgaatatgtcca 620  
 Db 117 CAGACTCCTTGTCTATCTTTTGGTAGAGAGATATGATTTCTCAAGTAT-CCAT 175  
 Qy 621 catcctaataccagatctctgtgatgtgtaccatacattcccaagaggttttgcataat 680  
 Db 176 GACCGAATACCCAGAGCCTCTGTAATATATTACCTTCCATGGCAAAAGGGACTTTACAGAT 235  
 Qy 681 gtgattatgttaaggtctgaatgaggagacaatcctgggttatccttgggtcag 740  
 236 GTGATTAACCTTAAGGATCTTGACATGAGG-GATTAACTGGATTTGCCAGGTGGGCCAG 294  
 Qy 741 ttaatacacaagaaggaggcag-----gaaggagagtcagagagaatgg 787  
 Db 295 TATAATCACAGAAATCTTAAGAAATGGAGAGCGCAGACAGAGTCAGAGAAAGATTG 354  
 Qy 788 agatataccatctcttaatttgaagatggagtgaggggccttgagccacaataatgca-g 846  
 Db 355 AAGGTCTACACCACCTGGCTTTGAAAATAGAGGAAGGGGCTGTGAGCCAGGAGTGCA 414  
 Qy 847 gtgtttttagaaggtgaaagccaaggaacggattctctctctagatctccgaa--- 903  
 Db 415 CTGCCTTTATGAGCTGGCAAAAACAAGAAACAATAATCTCCTCTATAGTTTCCAGAAAC 474  
 Qy 904 -ggaacacagctctctgacacatggatttcagctcagtcagtcacccatttcagactctg 960  
 Db 475 GAACACAAACCCCTCTGACACCTTGATTNTAGCCCACTAGAAATCCTTTTGCACCTCTG 532

RESULT 11  
 A0318555  
 LOCUS A0318555 526 bp DNA linear GSS 04-MAY-1999  
 DEFINITION RPCI11-90J12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-90J12,

DNA sequence.  
 ACCESSION A0318555  
 VERSION A0318555.1 GI:4051597  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 526)  
 Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K.,  
 Berry K., Granger D., Suh E., Wible C., de Jong P., and Venter J.C.  
 Use of human BAC End Sequences for Sequence-Ready Map Building  
 Unpublished (1998); 90J12.TJ  
 Other\_GSSs: RPCI11-90J12.TJ  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbe@tigr.org  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 1..526  
 /organism="Homo sapiens"  
 /db\_xref="GDB:753443"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-90J12"  
 /clone\_lib="RPCI-11"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RPCI11 Human Male BAC Library"  
 158 a 86 c 122 g 160 t

Query Match 11.9%; Score 121; DB 12; Length 526;  
 Best Local Similarity 59.3%; Pred. No. 1.8e-19;  
 Matches 246; Conservative 0; Mismatches 160; Indels 9; Gaps 2;  
 Qy 583 ctatgtgaggcagaataatgtcccccgaaataatgtccacatcctcaatcccaag-atctgt 641  
 Db 56 CTATGTAAGCGGAATAATGGACTTCCCAAAAGGTCCTCATCTCATCTCGAATCTGT 115  
 Qy 642 gcatatgttaccatacatgtccaaagaggttttgcaaatgtattgttaaggatcttg 701  
 Db 116 GAATATGTTACTTACATGTAAGAGGACTTTACGATGATGATTAAGTTAGATCTTG 175  
 Qy 702 aaatgagagacaaatcctgggttatccttgggtcagtttaatacacaagaagaggca 761  
 Db 176 AGATGTGGAGATTCTTCTGGATTATTTTGCATACAGAAATAACACAGAGTCATGATA 235  
 Qy 762 ggaaggagagtcagagagaagaatggaatacaccatgcttctaattttgaagatggagtg 821  
 Db 236 GAGATAGGTACTAGATTAAAGTCGCTAGTAGGAATATGATATAGAGA-----TT 287  
 Qy 822 aggggaccttgagccacaataatgcagggtgtttttagaagtggaagaaaggggaacgga 881  
 Db 288 GGTGTAATGGAGCTGTGGAGTGTGGCGCTTTCAGAGCTTGAAGAGCTGAGAGCGCAGAGAACAGG 347  
 Qy 882 ttctctctctagatctcgcgaaggaacacagctcttgcacatcaggttttcagctcagtg 941  
 Db 348 TTTTCCCTTGGAAATCTCTGAAGAGAACACAGCTCGCTGACATCTTTGATTTTGGCCCCATAA 407  
 Qy 942 caccatttcagactcttgacctcccaactataataataaacttggttatt 996

Db	211	CTAAGAGTCGCTATGCTGCTTTTGAAGGAGATGAAGGGG-----CAGGAATTA	158
Qy	844	caggtgtttttagaagggtgaaagccagggagcgattctctcttagagttctccggaa	903
Db	157	GGGTGGTCTCTAGAACTCTGGAAGGCAATGAATTTGATTTCTCCCTAGAGCTTTGAGAA	98
Qy	904	ggaacacagc-tcttgacacatgatttcagctcaagtgcacacattcagctctga	961
Db	97	GGAATGCGAGCTTGGCCACACCTTCATTTTAGACCAGTGAATGATTTAGACTTCTGA	38
Qy	962	ctctccacacataaaataataaaacttggtttt	996
Db	37	CTGCCAGACTGTAGATAATAAATGATATTTGTT	3
RESULT	13		
LOCUS	AG087298/7		
DEFINITION	Pan troglodytes DNA, clone: PTB-085013.R, genomic survey sequence		
ACCESSION	AG087298		
VERSION	AG087298.1 GI:16639100		
KEYWORDS	GSS; GSS (genome survey sequence).		
SOURCE	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male		
ORGANISM	BAC library clone:PTB-085013.R.		
REFERENCE	Pan troglodytes		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
TITLE	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.		
JOURNAL	BAC end sequences of Library PTB		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 670)		
TITLE	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.		
JOURNAL	Direct Submission		
COMMENT	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
	Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.		
PRIMERS			
LIBRARY	Sequencing: M13Rev		
VECTOR	: pKS145		
R.Site 1	: SacI		
R.Site 2	: SacI		
FEATURES	Location/Qualifiers		
source	1..670		
	/organism="Pan troglodytes"		
	/db_xref="taxon:9598"		
	/clone="PTB-085013.R"		
	/sex="male"		
	/cell_type="lymphoblast"		
	/clone_lib="PTB Chimpanzee Male BAC Library"		
BASE COUNT	176 a 180 c 121 g 193 t		
ORIGIN			
Query Match	11.4%	Score 115.8; DB 12; Length 670;	
Best Local Similarity	64.2%;	Pred. No. 3.7e-18;	
Matches	228; Conservative	0; Mismatches 112; Indels 15; Gaps 3	
Qy	577	cagggtctatggtgaggagaataatgtcccccgaataatgtccacatcctaat-ccccag	635
Db	526	CACGTGGTCTGGGAGGAGAGAAATAATGGGTCCCCCAGAAACATACATGCTTCGCA	467
Qy	636	atctgtgcatatgtttaccacatcattccaaagaggttttgcacaaatgtgattatgtaag	695
Db	466	ACTCTGACCTGTTTACTCAGCTGGCAGATGCTACTGTCATGCTGATTCAGTGAAGG	407

696 atcttgaatgaggaacacatctctgggttatctcttgggctcagtttaatcacaa--- 752  
 |||||  
 Db ATCTTGAGATGAGGAGGTTATCTCGATATTCTTGGATGAATCGATGCATCACAGGTT 347  
 |||||  
 QY 753 -----aaggagcgaaggagagatcagagagagaalgaagaatcattctc 802  
 |||||  
 Db CCTTATAGAAAGAGCGATGAGGGTCAAGGTCAGAGTCAGAGAAACTGGAAGATGGTACCTAGC 287  
 |||||  
 QY 803 taatttgaagatggagtgaggggccttggaccacaaatgcaggt-gttttlagaaggt 861  
 |||||  
 Db TGGCTTTTGAAGATAGAGGAAGGGCGCAAAACCAAGGAATGCAGGTGCTCTTAGAAGCT 227  
 |||||  
 QY 862 gaaaaagccaaaggaacgattctctctctagatctccgaagaagaaacacagctct 916  
 |||||  
 Db GGAAAAGTCAAAGGGAACTAGTTCTCCCTAGAGCCTCCAGAAAGGAGCATGACCCC 172

RESULT	14
B54722/c	
LOCUS	B54722
DEFINITION	CIT-HSP-384F12.TR CIT-HSP Homo sapiens genomic clone 384F12, DNA
ACCESSION	B54722
VERSION	B54722.1
KEYWORDS	Gt:2609056
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 634)  
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S.S., Linher,K., Golden  
K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.  
and Venter,J.C.  
REFERENCE  
AUTHORS  
TITLE  
Use of a random BAC End Sequence Database for Sequence-Ready Map

**JOURNAL  
COMMENT**

Building  
Unpublished (1997)  
Other\_GSSs: CIT-HSP-384F12.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadamset@igr.org  
Clones are available from Research Genetics (info@resgen.com) . BAC  
end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search.html)  
Seq primer: M13 Reverse  
Class.: BAC ends.

FEATURES	Location/Qualifiers				
source	1..634				
	/organism="Homo sapiens"				
	/db_xref="GBB:5378290"				
	/db_xref="taxon:9606"				
	/clone="384F12"				
	/clone_lib="CIT-HSP"				
	/sex="Male"				
	/cell_type="Sperm"				
	/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"				
BASE COUNT	161 a	154 c	118 g	201 t	

Query Match 11.3%; Score 115.4; DB 12; Length 634;  
Best Local Similarity 60.9%; Pred. No. 4.6e-18;  
Matches 282; Conservative 0; Mismatches 136; Indels 45; Gaps 4;

**Oy**      563    aagctcatcgtcgcagggtctatggttaggcagaataatgccccgaatatgtccaca    622  
         ||| | | | | | | | | | | | | | | | | | | | |  
**Db**      579    AAGTTTAAGCTTCAGGGCTCTTGTTGGTAGGCTGGATAACAGATCCTCAAAGATGTCCACA    520

Qy	623	tcttaataccaag-----atctgtgcataatgtaccatacaatgtccaaagaggttttg	675
Db	519	TCTTAATCCTAATCCCGAGAATCTATGAATATGTGCTTGCATGCGTAAAAAGAACTTTC	460
Qy	676	caaatgtgattatgtaaggaatcctgaatagagagacaatcctgggttaccctctggg	735
Db	459	CAAAATGCTATTAAGCTGAAGATCTTTGAGATAGGGAGAGATTATTCTSGATTATCCAAGTGTC	400
Qy	736	ctcaggttaataccaag-----aaaggagg	759
Db	399	CCCATATATAATCACAGGGTCTCTTATAGGAGACAGGAGAGTCCACAGAGAAATGCAAGG	340
Qy	760	cagggaaggagtcagagagagaatggaagataaccatcctctctaattttgaagatcgag	819
Db	339	ACAGAAGACAGAAGTCCAGCGGGTGTAAATAATGCCTCACTACATGCTGACTGCTTTCAGGATGGAA	280
Qy	820	tgaggggccttgagaccacaataatcagctgttttttagaaggaggaaagccaaggaacg	879
Db	279	AAAGGAGCCATGAGCCAGGAGCTAGTGGCGCTCTAGGAGCTGGAGAGCGCTGGCAACCC	220
Qy	880	gattctctctagaagtcctcgggaaggaacacagcctcttgacacatgatttcagctcagt	939
Db	219	AACTCCCTC-GAGAATCTCCGAAGGAAGACATTCOCG-CACTTTGTATTTTAGCTCAGC	162
Qy	940	gacacccatttcagactctgacctcccaactataaaataat	982
Db	161	GAAACTGATTGTGACTTCTCACCTCTTTGAACTGTAATAAT	119
RESULT	15		
AQ405885/c			
LOCUS			
DEFINITION	AQ405885	525 bp	DNA
	HS_5043_B2_F07_T7 RPEC1-11 Human Male BAC Library Homo sapiens		linear
VERSION	AQ405885		
ACCESSION	AQ405885.1	GI:4415873	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 525)		
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,		
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and		
	Hood,L.		

TITLE	JOURNAL MEDLINE COMMENT
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	PROC. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu	
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@edejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering_bac.htm">http://bacpac.med.buffalo.edu/ordering_bac.htm</a> ) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <a href="http://www.htsc.washington.edu">http://www.htsc.washington.edu</a> Plate: 619 row: L column: 14	

```
Seq primer: T7
Class: BAC ends
High quality sequence stop: 525.
Location/Qualifiers
1. .525
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="plate-619 Col-14 Row=L"
    /clone.lib="RPC1-11 Human Male BAC Library"
    /sex="male"
```

/note="vector: pBACE3.6; Site.1: EcoRI; Site.2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACE3.6 vector at EcoRI sites"  
BASE COUNT 111 a 139 c 109 g 160 t 6 others  
ORIGIN

Query Match	11.28;	Score 114.6;	DB 12;	Length 525;
Best Local Similarity	70.08;	Pred. No. 7.1e-18;		
Matches 224;	Conservative 0;	Mismatches 90;	Indels 6;	Gaps 5;
Qy 636	atctgtgcatagtttaccatacatgtccaaagagggttttgcaaatgtgattatgtttaagg	695		
Db 361	ACCTGTCAATATGTGACCTTTTCATGGCAAAAGAGACTTTGC-AGTGTGATTTGGATTGAGG	303		
Qy 696	atctgaaatgaggagacaatccctgggttatcctt-gtgggctcagtttaatacacaaagaa	754		
302	ATCTTGAGATGAGGAGATTATCTGGTGGCCCTAAAGTAATCACAGGGGTCTCTATGAGAC	243		
Qy 755	ggaggcaggaaggg-agagtcagagagagaatggaagataccatgtcttctaattttgaag	813		
Db 242	GGAGGCAGGAGGTCCAGAGTCACACAGAGACTGGAAGATGCCACGCTGTGGCTTTGAAG	183		
Qy 814	atgagtgaggggccttagccaaataatgcagg-tgtttttagaaggtagaaagccaa	872		
Db 182	GTGAAGAGGGGCCCATGAGCCAGGCATCCAGCAGCTTCCACAAGCTGGAAAAAGAAA	123		
Qy 873	gggaacggattctctctagagtcctccggaaggaacacacagctct--tgacacatggattt	930		
Db 122	GGAACAGACTCTCTCTGGAGCATCCAGAAGGAGACACAACCCCTGCTAATACCTTGATNT	63		
Qy 931	cagctcagtgacacccattt	950		
Db 62	TAGCCACGTGAGATCCATTT	43		

Search completed: May 19, 2002, 08:44:01  
Job time: 14234 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:52:07 ; Search time 11.75 seconds  
(without alignments)  
474.302 Million cell updates/sec

Title: US-09-724-583-2  
Perfect score: 818  
Sequence: 1 MCSLPMARYIILKYADOKAL.....QLTKSESPSARTKFFEQSW 152

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swissprot\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	260.5	31.8	178	1 IL1X_RAT	P25086 rattus norv
2	257.5	31.5	178	1 IL1X_MOUSE	P25085 mus musculus
3	256	31.3	177	1 IL1X_PIG	Q29056 sus scrofa
4	241	29.5	177	1 IL1X_RABIT	P26890 oryctolagus
5	238.5	29.2	177	1 IL1X_HUMAN	P18510 homo sapien
6	238	29.1	177	1 IL1X_HORSE	O18999 equus caball
7	232	28.4	174	1 IL1X_BOVIN	P18510 ovis aries
8	134.5	16.4	267	1 IL1B_MOUSE	P26889 sus scrofa
9	132	15.2	269	1 IL1B_SHEEP	P21621 ovis aries
10	124.5	15.2	269	1 IL1B_MOUSE	P10749 mus musculus
11	119.5	14.6	266	1 IL1B_CEREL	P51745 cervus elap
12	117	14.3	266	1 IL1B_BOVIN	P09428 bos taurus
13	112.5	13.8	268	1 IL1B_RAT	Q63264 rattus norv
14	111	13.6	266	1 IL1B_CAPHI	P79162 capra hircu
15	110.5	13.5	268	1 IL1B_RABIT	P14628 oryctolagus
16	106.5	13.0	268	1 IL1B_MACFA	P79162 macaca fasc
17	106.5	13.0	269	1 IL1B_CERTO	P46648 cercopithec
18	106.5	13.0	269	1 IL1B_MACMU	P48090 macaca mula
19	106.5	13.0	269	1 IL1B_MACNE	P51493 macaca neme
20	104.5	12.8	269	1 IL1B_HUMAN	P01584 homo sapien
21	94.5	11.6	267	1 IL1B_FELCA	P41687 felis silve
22	92	11.2	268	1 IL1B_HORSE	Q28386 equus caball
23	77	9.4	997	1 YPX2_CARFL	Q20256 caenorhabdi
24	76.5	9.4	520	1 CPY3_HUMAN	Q08477 homo sapien
25	71.5	8.7	4303	1 PKD1_HUMAN	P08161 homo sapien
26	71	8.7	2766	1 THYG_MOUSE	O08710 mus musculus
27	70.5	8.6	620	1 VLCS_MOUSE	O35488 mus musculus
28	70.5	8.6	827	1 GAG_IPMA	P11365 mouse intra
29	69.5	8.5	214	1 GTH7_ARATH	Q96324 arabidopsis
30	69	8.4	355	1 KLC3_HUMAN	Q9nsk0 homo sapien
31	69	8.4	520	1 CPY2_HUMAN	P78329 homo sapien
32	69	8.4	700	1 PURL_HALN1	Q9hr49 halobacteri
33	68.5	8.4	557	1 IGEB_MOUSE	P03975 mus musculus

34	67.5	8.3	271	1 IL1A_MACMU	P48089 macaca mula
35	67	8.2	665	1 V176_METTH	Q26278 methanobact
36	67	8.2	832	1 BGAL_ASPOF	P45592 asparagus o
37	66.5	8.1	271	1 IL1A_MACFA	P79340 macaca fasc
38	66.5	8.1	687	1 V541_GIALA	P52127 giardia lam
39	66	8.1	254	1 TPIS_BUCAP	Q59179 buchnera ap
40	66	8.1	290	1 MAB3_CAEEL	O18214 caenorhabdi
41	66	8.1	438	1 GSA_STRCO	Q9f2s0 streptomyce
42	66	8.1	619	1 KLC3_MOUSE	Q9db55 mus musculu
43	65	7.9	531	1 G6PI_SYNY3	P52983 synecocyst
44	65	7.9	3206	1 POLG_PSBMV	P29152 p genome po
45	64.5	7.9	967	1 SVA_BOMMO	P21894 bombyx mori

ALIGNMENTS

RESULT	1
IL1X_RAT	
ID	IL1X_RAT
AC	P25086;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	01-NOV-1995 (Rel. 32, Last annotation update)
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE	(IRAP).
GN	IL1RN OR IL-1RA.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91271363; PubMed=1828896;
RA	Eisenberg S.P., Brewer M.F., Verderber E., Heimdal P.,
RA	Brandhuber B.J., Thompson R.C.;
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1
RT	gene family: evolution of a cytokine control mechanism.";
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC	!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC	RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC	!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use. by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M63101; AAA41434.1; .
DR	PIR; C40956; C40956.
DR	HSP; P18510; IL1R.
DR	InterPro; IPR000975; Interleukin_1.
DR	Prfam; PF00340; IL1; 1.
DR	PRINTS; P000264; INTERLEUKIN1.
DR	SMART; SM00125; IL1; 1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
KW	Glycoprotein; Signal.
FT	SIGNAL 1 26
FT	CHAIN 27 178
FT	INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT	PROTEIN.
FT	DISULFID 92 142
FT	CARBOHYD 110 110
FT	N-LINKED (GLCNAC... ) (POTENTIAL).
SQ	SEQUENCE 178 AA; 20282 MW; F3A5754FB6C51B03 CRC64;

Query Match 31.8%; Score 260.5; DB 1; Length 178;  
Best Local Similarity 44.5%; Pred. No. 2.7e-20;  
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;  
QY 16 DQKALYTRDGLIVGDPVADNC-CAEKICTLPNRGLDRTKVPFIIGGSRCLACVETE 74



```
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L39849; AAA99424.1; -
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;

Query Match 31.3%; Score 256; DB 1; Length 177;
Best Local Similarity 40.5%; Pred. No. 7.8e-20;
Matches 62; Conservative 21; Mismatches 56; Indels 14; Gaps 5;

2 CSLPMARYIIKYADQKALYTRDGLLVGDPVADNC-CAEKICTLPNRLDRTKVP--IF 58
33 CRMQAFRIWDV---NOKTFYLRNQLVAGYLOGPNTKLEKIDVVPV-----PHFVF 82
59 LGIOGSRCLACVETEGPSIQLEDVNIIEYKGGEEATRTFFOSSSGSAFRLEAAWP 118
83 LGINGKGLCLSCVKSGDKMKLHLEAVNITDLRNSEQDKRRTFIRSDSGPTTSFSAACP 142
119 GWFLCGPAEPQPVOLTKSEPSAR-TKFFFEQ 150
143 GWFCLTALEADQPVGLTNTPKAAVKVKFFEQ 175

RESULT 4
IL1X_RABIT
ID IL1X_RABIT STANDARD; PRT; 177 AA.
AC P26890;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE (IRAP).
DE IL1RN OR IL1RA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=94165101; PubMed=7509813;
Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
Brewer M.T., Eisenberg S.P., Ng R.K.;
"Rabbit interleukin-1 receptor antagonist. Cloning, expression,
functional characterization, and regulation during intestinal
inflammation.";
J. Biol. Chem. 269:6962-6971(1994).
[2]
SEQUENCE FROM N.A.
Hamada H., Mulligan R.C.;
Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=93052512; PubMed=1427977;
Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
"Interleukin-1 receptor antagonist in inflammatory exudate cells of
rabbits. Production, purification and determination of primary
structure.";
Immunology 77:235-244(1992).
-!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
```

```
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S68977; AAB30093.1; -
DR EMBL: M57526; AAA31374.1; -
DR EMBL: D21832; BAA04860.1; -
DR PIR: A54377; A54377.
DR HSP: P18510; IL1R.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20214 MW; F5BC087F097FEEAF CRC64;

Query Match 29.5%; Score 241; DB 1; Length 177;
Best Local Similarity 39.2%; Pred. No. 2.9e-18;
Matches 60; Conservative 22; Mismatches 57; Indels 14; Gaps 5;

2 CSLPMARYIIKYADQKALYTRDGLLVGDPVADNC-CAEKICTLPNRLDRTKVP--IF 58
33 CRMQAFRIWDV---NOKTFYLRNQLVAGYLOGPNTKLEKIDVVPV-----PQLIF 82
59 LGIOGSRCLACVETEGPSIQLEDVNIIEYKGGEEATRTFFOSSSGSAFRLEAAWP 118
83 LGIOGKGLCLSCVKSGDKMKLHLEAVNITDLGNKEQDKRRTFIRNSGPTTFESASCP 142
119 GWFLCGPAEPQPVOLTKSEPS-ARTKFFFEQ 150
143 GWFCLTALEADQPVSLTNTPDSDSIVVTKFFQE 175

RESULT 5
IL1X_HUMAN
ID IL1X_HUMAN STANDARD; PRT; 177 AA.
AC P18510;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-
DE 1RA) (IRAP) (IL-1RN).
DE IL1RN OR IL1RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=90220867; PubMed=2139180;
Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
Slighom J.L., Berger A.E., Bienkowski M.J., Sun F.P., McEwan R.N.,
Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrichson R.L.,
Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
"Purification, cloning, expression and biological characterization of
an interleukin-1 receptor antagonist protein.";
Nature 344:633-638(1990).
[2]
SEQUENCE FROM N.A.
MEDLINE=90136921; PubMed=2137201;
```

RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,  
RA Hannum C.H., Thompson R.C.;  
RT "Primary structure and functional expression from complementary DNA  
RT of a human interleukin-1 receptor antagonist.";  
RL Nature 343:341-346(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91271363; PubMed=1828896;  
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,  
RA Brandhuber B.J., Thompson R.C.;  
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1  
RT gene family: evolution of a cytokine control mechanism.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92338323; PubMed=1385987;  
RA Leonard A., Gorman P., Carrier M., Griffiths S., Scotney H.,  
RA Sheer D., Solari R.;  
RT "Cloning and chromosome mapping of the human interleukin-1 receptor  
RT antagonist gene.";  
RL Cytokine 4:83-89(1992).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-97146044; PubMed=8992991;  
RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,  
RA Arend W.P., Smith M.F. Jr.;  
RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific  
RT and inducible regulatory regions.";  
RL J. Immunol. 158:748-755(1997).  
RN [6]  
RP SEQUENCE OF 26-45.  
RX MEDLINE-90136920; PubMed=2137200;  
RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,  
RA Heimdal P.L., Arnes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;  
RT "Interleukin-1 receptor antagonist activity of a human interleukin-1  
RT inhibitor.";  
RL Nature 343:336-340(1990).  
RN [7]  
RP SEQUENCE OF 26-52.  
RX MEDLINE-90354444; PubMed=2143761;  
RA Bienkowski M.J., Bessalu T.E., Berger A.E., Truesdell S.E.,  
RA Shelly J.A., Labore A.L., Zurcher-Neely H.A., Reardon I.M.,  
RA Heinrikson R.L., Chosay J.G., Tracey D.E.;  
RT "Purification and characterization of interleukin 1 receptor level  
RT antagonist proteins from FHP-1 cells.";  
RL J. Biol. Chem. 265:14503-14511(1990).  
RN [8]  
RP SEQUENCE FROM N.A. (INTRACELLULAR FORM).  
RX MEDLINE-91219436; PubMed=1827201;  
RA Haskill S., Martin G., van Le L., Morris J., Peace A., Biglier C.F.,  
RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;  
RT "cDNA cloning of an intracellular form of the human interleukin 1  
RT receptor antagonist associated with epithelium";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).  
RN [9]  
RP STRUCTURE BY NMR.  
RX MEDLINE-92297633; PubMed=1534997;  
RA Stockman B.J., Scchill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,  
RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;  
RT "Secondary structure and topology of interleukin-1 receptor  
RT antagonist protein determined by heteronuclear three-dimensional NMR  
RT spectroscopy.";  
RL Biochemistry 31:5237-5244(1992).  
RN [10]  
RP STRUCTURE BY NMR.  
RX MEDLINE-94320651; PubMed=8045306;  
RA Stockman B.J., Scchill T.A., Strakalaitis N.A., Brunner D.P.,  
RA Yem A.W., Deibel M.R. Jr.;  
RT "Solution structure of human interleukin-1 receptor antagonist  
RT protein.";  
RL FEBS Lett. 349:79-83(1994).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=94230368; PubMed=8175703;  
RA Vigers G.P.A., Caffes P., Evans P., Thompson R.C., Eisenberg S.P.,  
RA Brandhuber B.J.;  
RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A  
RT resolution.";  
RL J. Biol. Chem. 269:12874-12879(1994).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RX MEDLINE=95172072; PubMed=7867645;  
RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,  
RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;  
RT "Refined crystal structure of the interleukin-1 receptor antagonist.  
RT Presence of a disulfide link and a cis-proline.";  
RL Eur. J. Biochem. 227:838-847(1995).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.  
RX MEDLINE=97215904; PubMed=9062194;  
RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,  
RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;  
RT "A new cytokine-receptor binding mode revealed by the crystal  
RT structure of the IL-1 receptor with an antagonist.";  
RL Nature 386:194-200(1997).  
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS  
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT  
CC FORM).  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS  
CC PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -!- DATABASE: NAME=R&D Systems' cytokine source book;  
CC WWW="http://www.rndsystems.com/cyt\_cat/il1ra.html".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; M55646; AAA59138.1; -  
CC EMBL; M63099; AAB41943.1; -  
CC EMBL; X52015; CAA36262.1; -  
CC EMBL; X53296; CAA37386.1; -  
CC EMBL; X64532; CAA45832.1; -  
CC EMBL; U65590; AAB92268.1; -  
CC EMBL; U65590; AAB92270.1; -  
CC PIR; A30368; A30368.  
CC PIR; A37822; A37822.  
CC PIR; S08160; S08160.  
CC PIR; S08159; S08159.  
CC PIR; A40956; A40956.  
CC PIR; A39386; A39386.  
CC PDB; 1L1N; 30-APR-94.  
CC PDB; 2LRT; 15-OCT-94.  
CC PDB; 1LRP; 27-FEB-95.  
CC PDB; 1ILR; 07-FEB-95.  
CC PDB; 1LIT; 01-APR-95.  
CC PDB; 1IRA; 17-JUN-98.  
CC Aarhus/Ghent-2DPAGE; 7104; IEF.  
CC Aarhus/Ghent-2DPAGE; 7105; IEF.  
CC MIM; 147679; -  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC PRINTS; PRO0264; INTERLEUKIN1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1.  
KW Glycoprotein; Signal; Alternative splicing; 3D-structure.  
FT SIGNAL 1 25  
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST  
FT PROTEIN.



```

FT DISULFID      91   141
FT CARBOHYD     109   109
FT VARSPLIC       1    21
FT METCGRSHLITLLIFHS -> MAL (IN INTRACELLULAR ISOFORM).
SQ SEQUENCE     177 AA; 20055 MW; D1690776A7394057 CRC64;

Query Match          29.28; Score 238.5; DB 1; Length 177;
Best Local Similarity 40.9%, Pred.No.5.4e-18;
Matches 56; Conservative 18; Mismatches 56; Indels 7; Gaps 13;

QY 16 DOKALYTRDGQLLVDPVADNC-CAEKICTLPNRGLDRTKVPFIPIGIGSGRCLACVETE 74
Db :||| ||| ||| | ||| :| :||| || |||:::
44 NOKTYLRNNQVLAVGLQPNVNLEERIDVVPIE-----PHALEFLGIHGKMCILSCVKSG 98
QY 75 EGPISLOLEDNVNIELYKGGEATRTFFOSSAGFRLEAAWPCWFELCPAPQPQVOL 134
Db :||| ||| ||| :||| :||| :||| ||| ||| |||
99 DETRLQLEAVNTDLSENRRQDKRFATIRSDGPTTSFSASACPWFELCTAMEADQPVS 158
QY 135 TKSEPSAR-TKTFYEQ 150
Db : |||:::
159 TNMPDEGVMTKEYFEQ 175

RESULT 6
ILIX_HORSE
AC ILIX_HORSE STANDARD: PRT; 177 AA.
ID O18999; O77745;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROPEIN PRECURSOR (IL-1RA) (IL-1RN) (IRAP).
DE GN IL1BN OR IL1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RX [1]
SEQUENCE FROM N.A.
RP MEDLINE=97366446; PubMed=9223227;
RA Kato H., Ohashi T., Matsushiro H., Watarai T., Goitsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and functional expression of equine interleukin-1 receptor antagonist.";
RT Vet. Immunol. Immunopathol. 56:221-231(1997).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=98285942; PubMed=9622739;
RW Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 receptor antagonist and determination of its full-length cDNA sequence.";
RN Am. J. Vet. Res. 59:712-716(1998).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D83714; BAA22529.1; --
CC EMBL; U92482; AAC39257.1; -.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC PRINTS; PR00264; INTERLEUKIN1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Glycoprotein; Signal.

```

```

DR SMART; SM00125; IL1; 1
KW PROSITE; PS00253; INTERLEUKIN_1; 1
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 114 BY SIMILARITY.
FT CHAIN 115 267 INTERLEUKIN-1 BETA.
SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;

Query Match 16.4%; Score 134.5; DB 1; Length 267;
Best Local Similarity 31.2%; Pred. No. 7.3e-07;
Matches 30; Conservative 20; Mismatches 45; Indels 1; Gaps 1;

QY 54 KVPFLGIQGSCLACVETEGPSLQEDVNIEELYKGGEATRTFFQSSGSAFRLE 113
   1: 111: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Db 169 KIPVTGLIGKNLYSCVMKNTPTLQLEDID-PKRYPKRDMKRFVYFKTEIKNRVEF 227
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

QY 114 AAAPGFWGLCPAEPPOPVOLTKSEPSARTKFEF 149
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Db 228 SALYPNNWITTSQAQKPVFLGNSKGRQDITDTME 263
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

RESULT 9
IL1B_SHEEP STANDARD; PRT; 266 AA.
ID IL1B_SHEEP
DC P21621;
DT 01-WAY-1991 (Rel. 18, Created)
DT 01-WAY-1992 (Rel. 21, Last sequence update)
DT 30-WAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92119335; PubMed=1840515;
RX Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL DNA Seq. 1:423-426;(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088326; PubMed=2263490;
RX Fiskerstrand C., Sargan D.;
RT "Nucleotide sequence of ovine interleukin-1 beta.";
RL Nucleic Acids Res. 18:7165-7165(1990).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SPECIFIC AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X54796; CAA38566.1; -.
CC EMBL; X56972; CAA40293.1; -.
CC DDB; S13092; S13092.

```

```
DR PIR: S13810; S13810.
DR RX: S23010; S23010.
DR HSSP: P01584; 411B.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF02394; IL1_prop; 1.
DR PRINTS: PR00262; IL1_HBGF.
DR PRINTS: PR00264; INTERLEUKIN1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1.
DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 14 14 Y -> C (IN REF. 2).
FT CONFLICT 55 55 Q -> K (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 145 145 P -> L (IN REF. 2).
SQ SEQUENCE 266 AA; 30717 MW; BDED07B58224AB78 CRC64;

Query Match 16.1%; Score 132; DB 1; Length 266;
Best Local Similarity 25.4%; Pred. No. 1.3e-06;
Matches 34; Conservative 28; Mismatches 44; Indels 28; Gaps 3;

QY 16 DOKALYTRDGLLVGDPVADNCCAEKICTLPNRGLDR-----TKVPFIPLG 60
Db 127 EQKSL-----VLDSPCVLKALHLSQMSREVFVCFMSFVQGERDNKIPVALG 174
QY 61 IGGSRCLACVETEGPSQLQEDVNIIEELYKGGEATRTFFQSSGSAFRLFAAHPGW 120
Db 175 IRDKNLYLSCVKGGDTPTLQLEVD-PKVYPKRNKRKFVYKTEIKNTVEFSLYPMW 233
QY 121 FLCGPAEPQOPVOL 134
Db 234 YISTSQIEKPVFL 247

RESULT 10
IL1B_MOUSE STANDARD; PRT: 269 AA.
AC P10749;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87058957; PubMed=3491144;
RA Gray P.W., Glaister D., Chen E., Goeddel D.V., Pennica D.;
RT "Two interleukin 1 genes in the mouse: cloning and expression of the
cDNA for murine interleukin 1 beta.";
RL J. Immunol. 137:3644-3648(1986).
RN SEQUENCE FROM N.A.
RX MEDLINE=87117546; PubMed=3492706;
RA Telford J.L., Macchia G., Massone A., Carinci V., Palla E., Melli M.;
RT "The murine interleukin 1 beta gene: structure and evolution.";
RL Nucleic Acids Res. 14:9955-9963(1986).
RN SEQUENCE OF 118-139.
RX MEDLINE=88229074; PubMed=2967326;
RA Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Matthew J.B.,
RA Covington M., Lin Y.;
RT "Characterization of murine IL-1 beta. Isolation, expression, and
purification.";
RL J. Immunol. 140:3838-3843(1988).
```

```

[4]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92222792; PubMed=1807351;
RA van Oostrum J., Priestle J.P., Grutter M.G., Schmitz A.;
RT "The structure of murine interleukin-1 beta at 2.8-A resolution.";
RL J. Struct. Biol. 107:189-195(1991).
CC FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: M15131; AAA39276.1; -.
DR EMBL: X04964; CAA28637.1; -.
DR PIR: A24719; A24719.
DR PIR: S13029; S13029.
DR PDB: 8IIB; 15-OCT-94.
DR PDB: 2MIB; 31-JAN-94.
DR MGD: MGI:96543; I11B.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF02394; IL1_prop; 1.
DR PRINTS: PR00262; IL1_HBGF.
DR PRINTS: PR00264; INTERLEUKIN1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW 3D-structure.
FT PROPEP 1 117
FT CHAIN 118 269 INTERLEUKIN-1 BETA.
FT STRAND 123 129
FT TURN 130 131
FT STRAND 134 137
FT TURN 140 141
FT STRAND 143 146
FT TURN 150 154
FT STRAND 159 163
FT TURN 170 171
FT STRAND 173 179
FT TURN 180 181
FT STRAND 184 191
FT TURN 192 193
FT STRAND 194 201
FT TURN 204 206
FT HELIX 214 216
FT STRAND 217 222
FT STRAND 227 231
FT TURN 235 236
FT STRAND 238 242
FT STRAND 247 248
FT STRAND 250 252
FT STRAND 258 259
FT STRAND 262 266
SQ SEQUENCE 269 AA; 30931 MW; 734FA17B02ED87EE CRC64;
```

```

FT CHAIN 114 266 INTERLEUKIN-1 BETA.
SQ SEQUENCE 266 AA; 30629 MW; 4f40b4E6f0d9F060 CRC64;

Query Match 14.6%; Score 119.5; DB 1; Length 266;
Best Local Similarity 29.6%; Pred. No. 2.7e-05;
Matches 24; Conservative 22; Mismatches 3; Indels 1; Gaps 1;

QY 54 KVPFLGIGSGRCLACVETEGSLQEDVNTIEELKYGGEATRTFFFOSSGSAFRL 113
   11: 111: :: 111:: : 1111111: :: 111 111111: 1
Db 168 KIPVALGIRGKNQYLSCVKKGDTPLQLEED-PKVIAPRNKRKFVYKIEIKTV 226
   QY : 111:: : 111: 1
Db 227 SVLYPNWYISTSHPEEKPVFL 247

RESULT 12
IL1B_BOVIN STANDARD; PRT; 266 AA.
ID IL1B_BOVIN
AC P09428;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RX [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=85015591; PubMed=3262866;
RA Leong S.R., Flagg G.W., Lawman M., Gray P.W.;
RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta. ";
RT Nucleic Acids Res. 16:9054-9054(1988).
[2]
RX SEQUENCE FROM N.A.
RP MEDLINE=88318652; PubMed=3261832;
RA Malliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RA Gillis S., Cerretti D.P.;
RT "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT interleukin 1 beta complementary DNAs.";
Mol. Immunol. 25:429-437(1988).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR ENBL; M35589; AAA30585.1; -
DR ENBL; X12498; CAA31018.1; -
DR ENBL; M37211; AAA30584.1; -
DR PJR; JLU0010; ICBO1B.
DR PIR; S01380; S01380.

```

```

RESULT 14
IL1B_CAPHI
ID IL1B_CAPHI STANDARD: PRT: 266 AA.
AC P79162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) .
GN IL1B.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT "Molecular cloning and expression of caprine IL-1alpha and
RT IL-1beta.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBEJ databases..
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY) .
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 04:48:21 ; Search time 82.04 Seconds  
(without alignments)  
3053.951 Million cell updates/sec

Title: US-09-724-583-1  
Perfect score: 1020  
Sequence: 1 cagggatcagggttcaggga.....acctctaaaaaaaaaaaaa 1020

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Hit-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2.6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2.6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2.6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2.6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2.6/ptodata/2/ina/PCRUS.COMB.seq.\*  
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991.2	97.2	998	4	US-09-316-081-1
2	991.2	97.2	998	4	US-09-316-081-3
3	110.8	10.9	1282	4	US-09-417-455-4
4	110.8	10.9	1282	4	US-09-348-942-4
5	110.8	10.9	2648	4	US-09-417-455-6
6	110.8	10.9	2648	4	US-09-348-942-6
7	103.4	10.1	1710	3	US-09-000-630C-1
8	103.4	10.1	1710	3	US-08-862-730C-1
9	97.4	9.5	176373	3	US-09-128-155-17
c 10	97	9.5	246240	2	US-08-724-394A-20
c 11	97	9.5	246240	2	US-08-724-394A-21
c 12	97	9.5	246240	2	US-08-724-394A-22
13	95	9.3	462	3	US-08-798-414-1
14	95	9.3	462	4	US-09-131-247-1
15	95	9.3	474	1	US-08-476-860-9
16	95	9.3	474	1	US-08-910-733-9
17	95	9.3	474	2	US-08-910-884-9
18	95	9.3	514	1	US-08-284-784-41
19	95	9.3	514	2	US-08-854-811-41
20	95	9.3	531	2	US-08-809-185-1
21	95	9.3	534	3	US-09-000-630C-24
22	95	9.3	534	3	US-08-862-730C-24
23	95	9.3	543	1	US-08-422-655-1
24	95	9.3	579	1	US-08-476-860-12
25	95	9.3	579	1	US-08-910-733-12
26	95	9.3	579	2	US-08-910-884-12
27	95	9.3	602	1	US-08-459-811-1

28	95	9.3	602	1	US-08-459-092-1	Sequence 1, Appli
29	95	9.3	602	2	US-08-459-814-1	Sequence 1, Appli
30	95	9.3	602	2	US-08-425-232-1	Sequence 1, Appli
31	95	9.3	602	2	US-08-471-227-2	Sequence 2, Appli
32	95	9.3	603	1	US-08-484-598-1	Sequence 1, Appli
33	95	9.3	603	2	US-08-479-140-1	Sequence 1, Appli
34	95	9.3	603	3	US-08-477-143-1	Sequence 1, Appli
35	95	9.3	717	1	US-08-284-784-40	Sequence 40, Appl
36	95	9.3	717	2	US-08-854-811-40	Sequence 40, Appl
37	94	9.2	537	3	US-09-000-630C-27	Sequence 27, Appl
38	94	9.2	537	3	US-08-862-730C-27	Sequence 27, Appl
39	92.4	9.1	537	3	US-09-000-630C-25	Sequence 25, Appl
40	92.4	9.1	537	3	US-08-862-730C-25	Sequence 25, Appl
41	88.4	8.7	534	3	US-09-000-630C-26	Sequence 26, Appl
42	88.4	8.7	534	3	US-08-862-730C-26	Sequence 26, Appl
43	84.6	8.3	475	4	US-09-131-247-3	Sequence 3, Appli
44	84.6	8.3	1167	4	US-09-131-247-15	Sequence 15, Appl
45	84.6	8.3	1170	4	US-09-131-247-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-316-081-1  
; Sequence 1, Application US/09316081  
; Patent No. 6339141  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Dennis G.  
; APPLICANT: Pace, Ann M.  
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods  
; FILE REFERENCE: 28110/35659  
; CURRENT APPLICATION NUMBER: US/09/316,081  
; CURRENT FILING DATE: 1999-05-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (54)..(512)  
US-09-316-081-1

Query Match	97.2%	Score 991.2;	DB 4;	Length 998;
Best Local Similarity	99.7%	Pred. No. 9.4e-300;		
Matches	993;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0;
Qy	11	ggttcacgaactcaggatctgcagtgagaccagacaccactgattgcaggaatgtgtt	70	
Db	1	ggttcacgaactcaggatctgcagtgagaccagacaccactgattgcaggaatgtgtt	60	
Qy	71	ccctcccccagcaagatactacataataatgacagaccagagctctatacaca	130	
Db	61	ccctcccccagcaagatactacataataatgacagaccagagctctatacaca	120	
Qy	131	gagatggcagctgctggggagatcctctgtgcagacaactctgtgtgcagagaagatct	190	
Db	121	gagatggcagctgctggggagatcctctgtgcagacaactctgtgtgcagagaagatct	180	
Qy	191	gcacacttcttaacagagcttgaccgcacacgaagctcccaatttctcggagtcagg	250	
Db	181	gcacacttcttaacagagcttgaccgcacacgaagctcccaatttctcggagtcagg	240	
Qy	251	gagggagccctgctgcagatgtgtggagacagaagagggccttcctacagctgagag	310	
Db	241	gagggagccctgctgcagatgtgtggagacagaagagggccttcctacagctgagag	300	
Qy	311	atgtgaacattgagaaactgtacaaagtggtgaagagccacacgcttcacctttcc	370	
Db	301	atgtgaacattgagaaactgtacaaagtggtgaagagccacacgcttcacctttcc	360	

QY 371 agagcagctcaggtccgctcagcgttgaggtgaggtgctgctggtggtggttccctgt 430  
|||||  
Db 361 agagcagctcaggtccgctcagcgttgaggtgaggtgctgctggtggttccctgt 420  
|||||  
QY 431 gtggtccgag 490  
|||||  
Db 421 gtggtccgag 480  
|||||  
QY 491 gtaccaagtgtttactttgaacagagctgtgagagagagagagagagagagagagag 550  
|||||  
Db 481 gtaccaagtgtttactttgaacagagctgtgagagagagagagagagagagagagag 540  
|||||  
QY 551 tgcccccaaaacagctcaactgtcaggtgaggtgctatgtgaggtgagagagagagagag 610  
|||||  
QY 541 tgcccccaaaacagctcaactgtcaggtgaggtgctatgtgaggtgagagagagagagag 600  
|||||  
QY 611 aatatgtccacatcctaatacccaagatctgtgcatatgttaccatatacatgtcccaagag 670  
|||||  
Db 601 aatatgtccacatcctaatacccaagatctgtgcatatgttaccatatacatgtcccaagag 660  
|||||  
QY 671 ttttgcgaatgtattgttaaggatcttgaaatgaggtgagagagagagagagagagagag 730  
|||||  
Db 661 ttttgcgaatgtattgttaaggatcttgaaatgaggtgagagagagagagagagagagag 720  
|||||  
QY 731 gtgggtcagtttaatacacaag 790  
|||||  
Db 721 gtgggtcagtttaatacacaag 780  
|||||  
QY 791 ataccatgtcttaatttgaagatggagtgaggtgaggtgaggtgaggtgaggtgaggtgag 850  
|||||  
Db 781 ataccatgtcttaatttgaagatggagtgaggtgaggtgaggtgaggtgaggtgaggtgag 840  
|||||  
QY 851 ttttgaaggtggaag 910  
|||||  
Db 841 ttttgaag 900  
|||||  
QY 911 agctcttgacacatggatttcagctcagtgacacacacacacacacacacacacacacac 970  
|||||  
Db 901 agctcttgacacatggatttcagctcagtgacacacacacacacacacacacacacacac 960  
|||||

## RESULT 2

US-09-316-081-3  
; Sequence 3, Application US/09316081  
; Patent No. 6339141  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Dennis G.  
; APPLICANT: Pace, Ann M.  
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods  
; FILE REFERENCE: 28110/33569  
; CURRENT APPLICATION NUMBER: US/09/316.081  
; CURRENT FILING DATE: 1999-05-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(512)  
US-09-316-081-3

Query Match 97.2%; Score 991.2; DB 4; Length 998;  
Best Local Similarity 99.7%; Pred. No. 9.4e-300;  
Matches 993; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 ggttcaggaactcaggtatctgctgaggtgaggtgaggtgaggtgaggtgaggtgaggtg 70  
|||||  
Db 1 ggttcaggaactcaggtatctgctgaggtgaggtgaggtgaggtgaggtgaggtgaggtg 60  
|||||  
QY 71 cctcccccag 130  
|||||  
Db 61 cctcccccag 120  
|||||  
QY 131 gagatggcagctgctggtgagagatcctgtgagagagagagagagagagagagagagag 190  
|||||  
Db 121 gagatggcagctgctggtgagagatcctgtgagagagagagagagagagagagagagag 180  
|||||  
QY 191 gcacacttcttaacagaggtcttgaccgcacacaggtccccattttcttggggatccagg 250  
|||||  
Db 181 gcacacttcttaacagaggtcttgaccgcacacaggtccccattttcttggggatccagg 240  
|||||  
QY 251 gagggagcgcctgctgcatgtgtgagagagagagagagagagagagagagagagagag 310  
|||||  
Db 241 gagggagcgcctgctgcatgtgtgagagagagagagagagagagagagagagagagag 300  
|||||  
QY 311 atgtgaacatgtagagagatgtacaaaaggtgtgagagagagagagagagagagagagag 370  
|||||  
Db 301 atgtgaacatgtagagagatgtacaaaaggtgtgagagagagagagagagagagagagag 360  
|||||  
QY 371 agagcagctcaggtccgctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 430  
|||||  
Db 361 agagcagctcaggtccgctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 420  
|||||  
QY 431 gtggccgagcag 490  
|||||  
Db 421 gtggccgagcag 480  
|||||  
QY 491 gtaccaagtgttactttgaacagagctgtgaggtgaggtgaggtgaggtgaggtgaggtg 550  
|||||  
Db 481 gtaccaagtgttactttgaacagagctgtgaggtgaggtgaggtgaggtgaggtgaggtg 540  
|||||  
QY 551 tgcccccaaaacagctcaactgtcaggtgaggtgaggtgaggtgaggtgaggtgaggtgag 610  
|||||  
Db 541 tgcccccaaaacagctcaactgtcaggtgaggtgaggtgaggtgaggtgaggtgaggtgag 600  
|||||  
QY 611 aatatgtccacatcctaatacccaagatctgtgcatatgttaccatatacatgtcccaagag 670  
|||||  
Db 601 aatatgtccacatcctaatacccaagatctgtgcatatgttaccatatacatgtcccaagag 660  
|||||  
QY 671 ttttgcgaatgtattgttaaggatcttgaaatgaggtgaggtgaggtgaggtgaggtgag 730  
|||||  
Db 661 ttttgcgaatgtattgttaaggatcttgaaatgaggtgaggtgaggtgaggtgaggtgag 720  
|||||  
QY 731 gtgggtcagttttaaatacacaagagagagagagagagagagagagagagagagagagag 790  
|||||  
Db 721 gtgggtcagttttaaatacacaagagagagagagagagagagagagagagagagagagag 780  
|||||  
QY 791 ataccatgtcttaatttgaagatggagtgaggtgaggtgaggtgaggtgaggtgaggtgag 850  
|||||  
Db 781 ataccatgtcttaatttgaagatggagtgaggtgaggtgaggtgaggtgaggtgaggtgag 840  
|||||  
QY 851 ttttgaaggtggaag 910  
|||||  
Db 841 ttttgaag 900  
|||||  
QY 911 agctcttgacacatggatttcagctcagtgacacacacacacacacacacacacacacac 970  
|||||  
Db 901 agctcttgacacatggatttcagctcagtgacacacacacacacacacacacacacacac 960  
|||||

## RESULT 3

US-09-417-455-4  
; Sequence 4, Application US/09417455  
; Patent No. 6294655



```
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Face, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(537)
US-09-417-455-4
```

```
Query Match      10.9%; Score 110.8; DB 4; Length 1282;
Best Local Similarity 58.6%; Pred. No. le-24;
Matches 231; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

QY 81 ggcaagatactacataattaaatgcagaccagagagctctatcacagaagatggcca 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 ggcgtgtgtctccgaatgaaggactcggcattgaagggtcttattctgcataatacca 146

QY 141 gctgtgtgtggagatcctgttgacagacaactgctgt---gcagagaagatctgcacact 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 gcttctagtggaggtgtcatgcagggaaggtcattaaagggtgaagagatcagcgtgt 206

QY 198 tcctaacagaggtcttgaccgcaccaaggtccctcttctctgggtatccaggaggag 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 ccccaatcgtgtgtgtggtgcagcgtgtccctctctcctcctcctcctcctcctcctcct 266

QY 258 ccgctgtcctgtgagatcgttgagacagagagggccttccctacagctggagatgtgaa 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 ccagtgcctgtcatgtgggtg---gggcaggagcgcgactctaacactagagccagtga 323

QY 318 cattgaggaactgtacaaagtgtgaagagccacacgcttccctcttccagagcag 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 324 catcatgagctctatcttgggtcccaaggaatccaagagcttcaactctaccgcggga 383

QY 378 ctcaaggtccgcttcaggtctgaggtgtgaggtgtgaggtgtgaggtgtgaggtgtgagcc 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 catggggctcaactccagcttcgagtcggtcgtcctaccggggtgttctctgtgacggt 443

QY 438 ggcagagcccccagcagctacagctcaccaag 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 444 gcctgaagccgactcagcgtgtcagactcaccag 477
```

RESULT 4

```
US-09-348-942-4
; Sequence 4, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(537)
US-09-348-942-4
```

```
Query Match      10.9%; Score 110.8; DB 4; Length 1282;
Best Local Similarity 58.6%; Pred. No. le-24;
Matches 231; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

QY 81 ggcaagatactacataattaaatgcagaccagagagctctatcacagaagatggcca 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 ggcgtgtgtctccgaatgaaggactcggcattgaagggtcttattctgcataataacca 146

QY 141 gctgtgtgtggagatcctgttgacagacaactgctgt---gcagagaagatctgcacact 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 gcttctagtggaggtgtcatgcagggaaggtcattaaagggtgaagagatcagcgtgt 206

QY 198 tcctaacagaggtcttgaccgcaccaaggtccctcttctctgggtatccaggaggag 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 ccccaatcgtgtgtgtggtgcagcgtgtccctctcctcctcctcctcctcctcctcctcct 266

QY 258 ccgctgtcctgtgagatcgttgagacagagagggccttccctacagctggagatgtgaa 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 ccagtgcctgtcatgtgggtg---gggcaggagcgcgactctaacactagagccagtga 323

QY 318 cattgaggaactgtacaaagtgtgaagagccacacgcttccctcttccagagcag 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 324 catcatgagctctatcttgggtcccaaggaatccaagagcttcaactctaccgcggga 383

QY 378 ctcaaggtccgcttcaggtctgaggtgtgaggtgtgaggtgtgaggtgtgaggtgtgagcc 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 catggggctcaactccagcttcgagtcggtcgtcctaccggggtgttctctgtgacggt 443

QY 438 ggcagagcccccagcagctacagctcaccaag 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 444 gcctgaagccgactcagcgtgtcagactcaccag 477
```

RESULT 5





Db 478 CCTGCCCTGGCTGTCTCTGCACAGCACTGGAGGCCGACCGCCTGTGAGCCTCAACA 537

Qy 470 a 470

Db 538 A 538

# RESULT 9

US-09-128-155-17/c

; Sequence 17, Application US/09128155

; Patent No. 6117654

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; TITLE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/09/128,155

; EARLIER FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650

; EARLIER FILING DATE: 1998-07-02

; EARLIER APPLICATION NUMBER: US 60/054,646

; EARLIER FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 176373

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(176373)

; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-17

Query Match 9.5%; Score 97.4; DB 3; Length 176373;  
Best Local Similarity 62.1%; Pred. No. 2.9e-19;  
Matches 259; Conservative 0; Mismatches 141; Indels 17; Gaps 6;

Qy 585 atggtaggcagaataatgtcccccgaataatgtccacatctcctcccaagat-ctgtgc 643

Db 160498 ATGATAGGCGAATAATGGCACCCGCGAAATGTCCACATTTCAATCCCGAGCCGTGTGT 160439

644 atagtgtaccacacatgtcccaagaggttttgcacatgtgatt-atgttaaggtatcttga 702

160438 ATATGTTACATGACATACGACAAAGGGACITTTGCATCTGTGATTAAAGTTAAGCCTCTTTG 160379

Qy 703 aatgaaggagacaatcctcgtggttatcctgtgggtcagtttaatacacaag-----a 753

Db 160378 AGACGGGAGAGTATCTTGGATATTGACGTGAGCCCGATGTAATTTGCAAGCGTTCTTATA 160319

Qy 754 aggaggcagaagggagagtcagagagagaatggaagataccatgcttcaattttgaag 813

Db 160318 TGTGAAGAGGAAGCAGGAGGTCAGACAAAGCAGTGTGAGAAACCCCAAGCAGCGA 160259

Qy 814 atggagtaggggcttgagcccaacaaatgcaggt-gtttttagaaggttgaaagccaa 872

Db 160258 AGATGGGAGTGGCCACTAGCCAAAGGAATGCAGGTGGCCTCTGGAAGCTGGAAGGCGAA 160199

Qy 873 gggaacggattctctctatagttctcgggaaggaa--cacagctcttgacacatggattt 930

Db 160198 GGAAATTGACTTCCCTTAGAGCCTCCCAAGCAATGCTATCCTGCTGATACCTTTGATT 160139

Qy 931 cagctcagtgacacccatttcagactcttgacctcgcacacataataataataaac 987

Db 160138 TGGCCCGAGTGACACATTTCCAGA---CTGACCTCCATAACTGCAAGATAATACATT 160085

# RESULT 10

US-08-724-394A-20/c

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.  
; APPLICANT: Kronmal, Gregory S.  
; APPLICANT: Lauer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el  
; TITLE OF INVENTION: Sequences and Antibodies Thereto  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 017957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..246240  
; OTHER INFORMATION: /note= "HLA-H. CONTIG"

US-08-724-394A-20

Query Match 9.5%; Score 97; DB 2; Length 246240;  
Best Local Similarity 62.1%; Pred. No. 4.7e-19;  
Matches 259; Conservative 0; Mismatches 140; Indels 18; Gaps 6;

Qy 585 atggtaggcagaataatgtcccccgaataatgtccacatcctcaatcccaagatctgtgca 644

Db 37190 AGGTTAGCTGATGTTGTCTCCCAAGATATCCATGCTCTAATCCCGAGAACCTGTAAA 37131

Qy 645 tatgttaccatacatgtcccaagaggttttgcacaaatgtattatgttaagagatcttga 704

Db 37130 TATATTACCTTATATGACAAAAGGACCTTACATGTTTAAATAA-GTTAAGAATTTTGAGA 37072

Qy 705 tgaggaacaaatcctcgtggttacccttgggtc-agttaatacacaag-----aagg 756

Db 37071 TGGGCAGATTTTCTCAATTTTGCAGATGGGCCCTAGTGTATATCAAGGGTCTCTTATA 37012

Qy 757 aggcaggaagggagagtcagagagagaatggaagataccatgctctctaattttgaagatg 816

Db 37011 GAGACAGGCAAGAGAGTCAGAAATAAGAGAAAATACCTTCAAGATGTTACACTGTGGCTT 36952

Qy 817 gagtggag-----ggccttgagccacaacatgcaggtgttttttagaaggtggaagacc 870

Db 36951 TAAGTGTGAGAAAGGCCAAGAGCCAAAATATGAGTGGTCTACTACAAGCT-GAAAGCAA 36893

Qy 871 aaggggaacgattctcctctagagctcccggaagaaacacagc--tcttgacacatggat 928

Db 36893

```

Db 36892 AAAGAAATGAGATTTTCCCTAAAGCCTCTGGAGGGGGCAACAACCTTGCCAAATACCTTTGAT 36833

Qy 929 ttccagctcagtgacacccatttcagactcttgacctcccaactataataataaa 985
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 36832 TTTGGCTCAGTGAACCCATTTTGGAGCTTCTGACCTTTAGAATTGTAATAATAATAA 36776

RESULT 11
US-08-724-394A-21/C
: Sequence 21, Application US/0874394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kronmal, Gregory S.
: APPLICANT: Lauer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
: TITLE OF INVENTION: Sequences and Antibodies Thereeto
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A.
: REGISTRATION NUMBER: 35,136
: REFERENCE/DOCKET NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 246240 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..246240
: OTHER INFORMATION: /note= "HLA-H-CONTIG"
: US-08-724-394A-21

Query Match 9.5%; Score 97; DB 2: Length 246240;
Best Local Similarity 62.1%; Pred No 4.7e-19;
Matches 259; Conservative 0; Mismatches 140; Indels 18; Gaps 6;

Qy 585 atggtaggacagaataatgtcccccgaaatatgtccacatctctaataccccaaagatctgtgca 644
Db 37190 AGSGTAGGCTGAATGTGTGTCTCCAAAGATATCCATGTCTTAATCCCCAGAACTGTAAA 37131
Qy 645 tatgtaccatcacatgtccaaagaggttttgcaaatgtgattatgttaagatcttgaaa 704
Db 37130 TATATACCTTATATGACAAAGGACTTTACATGTTTAAATAA-GTTAAGAAATTTTGACA 37072
Qy 705 tgaggagacaaatcgtgggttatctcttggggctc-agtttaatacacaag-----aagg 756
  || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```









GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:51:47 ; Search time 24.69 Seconds  
(without alignments)  
900.502 Million cell updates/sec

Title: US-09-724-583-2  
Perfect score: 818  
Sequence: 1 MCSLPMARYIIKYADOKAL.....QLTKSEPSARTKFFFEQSW 152

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL-17.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	592	72.4	144	Q9BYX1	Q9byx1 homo sapien
2	309	37.8	156	Q9JIG2	Q9jig2 mus musculus
3	307	37.5	155	Q9QYX1	Q9qyx1 mus musculus
4	283	34.6	155	Q9QYH0	Q9qyh0 homo sapien
5	257.5	31.5	159	Q90207	O70207 mus musculus
6	248	30.3	176	Q9BEH0	Q9beh0 canis famil
7	245	30.0	177	Q9GMZ4	Q9gmz4 tursiops tr
8	238.5	29.2	143	Q9UPC0	Q9upc0 homo sapien
9	238.5	29.2	180	Q14628	Q14628 homo sapien
10	238	29.1	176	Q9GKK2	Q9gkk2 canis famil
11	177.5	21.7	169	Q9NZH8	Q9nzh8 homo sapien
12	176	21.5	157	Q9UHA5	Q9uha5 homo sapien
13	172	21.0	183	Q9D626	Q9d626 mus musculus
14	169	20.7	158	Q9UHA7	Q9uha7 homo sapien
15	164.5	20.1	172	Q9HBF3	Q9hbf3 homo sapien
16	156	19.1	176	Q9HBF2	Q9hbf2 homo sapien
17	155.5	19.0	192	Q9UHA6	Q9uha6 homo sapien
18	155.5	19.0	218	Q9NZH6	Q9nzh6 homo sapien
19	155.5	19.0	218	Q9HBF3	Q9hbf3 homo sapien

20	154.5	18.9	267	13	Q93909	O73909 gallus gall
21	154	18.8	160	11	Q9JIA2	Q9jia2 mus musculus
22	137.5	16.8	267	6	Q29082	Q29082 sus scrofa
23	135.5	16.6	283	13	Q9PVZ5	Q9pvz5 xenopus lae
24	123	15.0	118	6	Q9TSJ0	Q9tsj0 equus caball
25	120.5	14.7	266	11	Q9WVG1	Q9wvg1 cavia porce
26	113	13.8	266	6	Q9TRK1	Q9trk1 cursiops tr
27	110	13.4	260	13	Q9YGD3	Q9ygd3 oncorhynch
28	105	12.8	254	13	Q9PTI2	Q9pti2 oncorhynch
29	104.5	12.8	153	4	Q43645	Q43645 homo sapien
30	95.5	11.7	65	6	Q9TV37	Q9tv37 equus caball
31	92.5	11.3	276	13	Q57398	Q57398 cyprinus ca
32	92.5	11.3	276	13	Q9PW18	Q9pw18 cyprinus ca
33	91.5	11.2	269	6	Q9XS77	Q9xs77 trichosurus
34	89	10.9	3623	4	Q60494	Q60494 homo sapien
35	84.5	10.3	299	11	Q60800	Q60800 mus musculus
36	84.5	10.3	1313	4	Q5C0C9	Q5c0c9 homo sapien
37	81.5	10.0	272	13	Q9DDF2	Q9ddf2 cyprinus ca
38	80	9.8	381	2	Q9RWJ7	Q9rwj7 streptococc
39	80	9.8	1092	2	Q54099	Q54099 streptococc
40	78.5	9.6	272	13	Q9DDF3	Q9ddf3 cyprinus ca
41	77.5	9.5	843	6	Q9TUQ3	Q9tud3 sus scrofa
42	76	9.3	463	10	Q43183	Q43183 solanum tub
43	76	9.3	1117	2	Q53971	Q53971 streptococc
44	75	9.2	64	13	Q98SG5	Q98sg5 scopthalmu
45	73.5	9.0	520	4	Q60634	Q60634 homo sapien

## ALIGNMENTS

RESULT 1					
Q9BYX1					
ID	Q9BYX1	PRELIMINARY:	PRT:	144 AA.	
AC	Q9BYX1				
DT	01-JUN-2001 (Tremblrel. 17, Created)				
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)				
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)				
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST FKSG75.				
GN	FKSG75.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wang Y., Li T., Gong L.;				
RT	"Identification and characterization of FKSG75, a novel member of the interleukin-1 family.";				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY026753; AAK01948.1; .				
KW	Receptor.				
SQ	SEQUENCE 144 AA; 15811 MW; 8733B16D6F118BB9 CRC64;				

Query Match	72.4%	Score 592;	DB 4;	Length 144;
Best Local Similarity	98.2%;	Pred. No. 8e-55;		
Matches 111;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	40	EKICTLPNRLDRTKVPIFLIGTGGSRCLACVETEGPSQLQEDVNIIELYKGGEATRF	99	
Db	32	EKICTLPNRLDRTKVPIFLIGTGGSRCLACVETEGPSQLQEDVNIIELYKGGEATRF	91	
QY	100	TFEQSSGSAPFLAAAWPGWELCGPAPQVPVLTKESEPSARTKFFFEQSW	152	
Db	92	TFEQSSGSAPFLAAAWPGWELCGPAPQVPVLTKESEPSARTKFFFEQSW	144	

RESULT 2					
Q9JIG2					
ID	Q9JIG2	PRELIMINARY:	PRT:	156 AA.	
AC	Q9JIG2				
DT	01-OCT-2000 (Tremblrel. 15, Created)				

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INTERLEUKIN-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG 1).  
 GN IL1HL1  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA DeBets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,  
 RA Kastelein R.A.;  
 RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=TONGUE, AND STOMACH;  
 MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Baldarelli R., Barsh G.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ringwald L., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Willing L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AF230378; AAF91275.1; -  
 DR EMBL: AK009741; BAB26471.1; -  
 DR EMBL: AK008972; BAB26002.1; -  
 DR MGD: MGI:1859325; Il1hl1.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1; 1.  
 DR SEQUENCE 156 AA; 17136 MW; A4D1EE2F93CF77A7 CRC64;  
  
 Query Match 37.8%; Score 309; DB 11; Length 156;  
 Best Local Similarity 45.2%; Pred. No. 6.3e-25;  
 Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;  
  
 QY 1 MCSLPARYIYIKYADQALYTRDQQLLYGDPVADNCC-AEKICTLPNRLDRTKVPFL 59  
 Db 1 MWVLSALCFRMDKALKVLYHNQLLAGLHAERKVEISVVPNRALDASLSPLVL 60  
  
 QY 60 GIGGSRCLACVETEEGSLQLEDVNIIELYKGGEATRTFFOSSGSAFLEAAWPG 119  
 Db 61 GVQGGSQLSC-GTEKGPILKEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPG 119  
  
 QY 120 WFLCGPAEQPQVLTKEPSA----RTKFFFEQ 150  
 Db 120 WFLCTSPADQPVRLTQIPEDPAWDAPITDFYFQQ 154  
  
 RESULT 3  
 ID Q9QYI1 PRELIMINARY; PRT; 155 AA.  
 AC Q9QYI1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INTERLEUKIN-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG 1).  
 GN IL1HL1 OR IL1L1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092888; PubMed=10625660;  
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,  
 RA Sims J.E.;  
 RT "Four New Members Expand the IL-1 Superfamily.";  
 RL J. Biol. Chem. 275:1169-1175(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99443727; PubMed=10512743;

DE IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).  
 GN IL1HL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barton J.L., Nicklin M.J.H.;  
 RT "IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed  
 in Trophoblasts and Macrophages.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20209405; PubMed=10744718;  
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
 RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,  
 RA Young P.R.;  
 RT "Identification and initial characterization of four novel members of  
 the interleukin-1 family.";  
 RL J. Biol. Chem. 275:10308-10314(2000).  
 DR EMBL: AJ250429; CAF59831.1; -  
 DR EMBL: AF200495; AAF69251.1; -  
 DR RSP: P18510; IL1L1.  
 DR MGD: MGI:1859325; Il1hl1.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1; 1.  
 DR SEQUENCE 155 AA; 17004 MW; A4B1770F2E12533A CRC64;  
  
 Query Match 37.5%; Score 307; DB 11; Length 155;  
 Best Local Similarity 47.8%; Pred. No. 1e-24;  
 Matches 66; Conservative 20; Mismatches 46; Indels 6; Gaps 3;  
  
 QY 18 KALYTRDQQLLYGDPVADNCC-AEKICTLPNRLDRTKVPFLGIGGSRCLACVETE 76  
 Db 17 KVLVLYHNQLLAGLHAERKVEISVVPNRALDASLSPLVLGVQGSQCLSC-GTEK 75  
  
 QY 77 PSLQLEDVNIIELYKGGEATRTFFOSSGSAFLEAAWPGVFLCGPAEQPQVLT 136  
 Db 76 PTLKLEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGVFLCTSPADQPVRLTQ 135  
  
 QY 137 ESEPSA----RTKFFFEQ 150  
 Db 136 IPEDPAWDAPITDFYFQQ 153  
  
 RESULT 4  
 ID Q9UBH0 PRELIMINARY; PRT; 155 AA.  
 AC Q9UBH0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE FILL DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR  
 ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).  
 GN IL1HL1 OR IL1L1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092888; PubMed=10625660;  
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,  
 RA Sims J.E.;  
 RT "Four New Members Expand the IL-1 Superfamily.";  
 RL J. Biol. Chem. 275:1169-1175(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99443727; PubMed=10512743;

```
RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,  
RA Dimnac R., Ford J.E.;  
RT "IL1H1: A Novel Interleukin-1 Receptor Antagonist Gene.";  
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;  
RT "A tissue specific interleukin-1 receptor antagonist homolog from the  
RT IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Barton J.L., Herbst R., Bosio D., Nicklin M.J.H.;  
RT "A tissue specific interleukin-1 receptor antagonist homolog from the  
RT IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20322477; PubMed=10866108;  
RX Mulero J.J., Nelken S.T., Ford J.E.;  
RT "Organization of the Human Interleukin-1 Receptor Antagonist Gene  
RT IL1H1.";  
RL Immunogenetics 51:425-428(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,  
RA Kastelein R.A.;  
RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA EMBL; AF201830; AAF25210.1; -  
DR EMBL; AF186094; AAF02757.1; -  
DR EMBL; AJ242737; CAB58822.1; -  
DR EMBL; AJ242738; CAB59823.1; -  
DR EMBL; AJ271338; CAB67704.1; -  
DR EMBL; AF216693; AAF76981.1; -  
DR EMBL; AF230377; AAF91274.1; -  
DR HSSP; P18510; IL1R.  
DR InterPro; IPR000975; Interleukin_1.  
DR SMART; SM00125; IL1; 1.  
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.  
KW Receptor.  
SQ SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;  
  
Query Match 34.6%; Score 283; DB 4; Length 155;  
Best Local Similarity 45.7%; Pred. No. 3.5e-22;  
Matches 63; Conservative 20; Mismatches 49; Indels 6; Gaps 3;  
  
Db 18 KALYTRDQGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFLFGIOGSRCLACVETE 76  
17 KVLVHNNQLLAGLHAGVKGEEISVVPNRLDASLSPVILGVGGSCQLSCGVGQE- 75  
17 PSLOLEDVNTIEELKGGEEATRTFFQSSSGSAFRLAAAWPGWFLCGPAEPQPVOLTK 136  
76 PTLTLEPVMELYLGAKESEFTFYRDMGLTSSFSFSAAYPGWFLCTVPEADQVRLTQ 135  
  
QY 137 ESE-----PSARTKFEYEQ 150  
Db 136 LPENGWGNAPITDFYFQQ 153  
  
RESULT 5  
O70207 PRELIMINARY; PRT; 159 AA.  
AC O70207;  
DT 01-AUG-1998 (TEMBLrel. 07, Created)  
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
DE INTRACELLULAR INTERLEUKIN-1 RECEPTOR ANTAGONIST.  
GN IL1RN.  
OS Mus musculus (Mouse).  
  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVBXDBA/1 LACJ;  
RX MEDLINE=98209757; PubMed=9550387;  
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;  
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning  
RT and protein expression of intracellular isoform and tissue  
RT distribution of secreted and intracellular IL-1 receptor antagonist in  
RT vivo.";  
RL J. Immunol. 159:5905-5913(1997).  
DR EMBL; AF001795; AAC15251.1; -  
DR HSSP; P18510; IL1RA.  
DR MGD; MGI:96547; IL1rn.  
DR InterPro; IPR000975; Interleukin_1.  
DR Pfam; PF00340; IL1; 1.  
DR SMART; SM00125; IL1; 1.  
DR PROSITE; PS00253; INTERLEUKIN_1; 1.  
SQ SEQUENCE 159 AA; 17995 MW; A7CD35D137846222 CRC64;  
  
Query Match 31.5%; Score 257.5; DB 11; Length 159;  
Best Local Similarity 44.5%; Pred. No. 1.7e-19;  
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;  
  
QY 16 DOKALYTRDQGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFLFGIOGSRCLACVETE 74  
26 NOKTFYLRNNQLIAGVLOGPNIKLEEKIDMVP---IDLHSV--FLGIHGKLCISCAKSG 80  
75 EGPSLOLEDVNTIEELKGGEEATRTFFQSSSGSAFRLAAAWPGWFLCGPAEPQPVOL 134  
81 DDIKLQLEEVNITDLSKNKEEDKRTFTIRSEKPTTSFSSAACPGWFLCTTLEADREVSL 140  
135 TK-ESEPSARTKFEYEQ 150  
141 TNTPEELIVTKFYFOE 157  
  
RESULT 6  
O9BEH0 PRELIMINARY; PRT; 176 AA.  
AC O9BEH0;  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shin I.-S., Youn H.-Y.;  
RT "Molecular cloning of canine interleukin-1 receptor antagonist (IL-  
RT 1ra).";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY026462; AAK01472.1; -  
KW Receptor.  
SQ SEQUENCE 176 AA; 19922 MW; 8486CA54A240212B CRC64;  
  
Query Match 30.3%; Score 248; DB 6; Length 176;  
Best Local Similarity 39.7%; Pred. No. 2e-18;  
Matches 60; Conservative 20; Mismatches 61; Indels 10; Gaps 4;  
  
QY 2 CSLPMARYIHKYADQKALYTRDQGLLVGDPVADNCC-AEKICTLPNRLDRTKVPFLG 60  
33 CRMQAFRIMDV---NOKTFYLRNNQLVAGVLOGSNKLEEKLDVVPE-----PHAVELG 84  
61 IOGGSRLACVETEFGPSLOLEDVNTIEELKGGEEATRTFFQSSSGSAFRLAAAWPGW 120  
Mus musculus (Mouse).
```



```

Best Local Similarity 40.9%; Pred. No. 2e-17;
Matches 56; Conservative 18; Mismatches 56; Indels 7; Gaps 3;

QY 16 DOKALYTRDQGLLVGDPVADNC-CAEKICTLPNRLDRTKVPFLGIGGSRCLACVETE 74
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 47 NOKTYFLRNQLVAGYLOGPNVNLKEDIKDVPIE-----PHALFLGHHGKMKLSCVKS 101

QY 75 EGPSIQLEDVNIIEELKYGGEATRTFFQSSGSAFRLEAAWPGWFLCGPAEPPOPVOL 134
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 102 DETRLQLEAVNTLDSKRNQKRFATIRSDSGPTTSFSAACPGWFLCTAMEADQPVSL 161

QY 135 TKESEPSAR-TKPYFEQ 150
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 162 TNMPDEGVMTKPYFOE 178

RESULT 10
ID Q9GKK2 PRELIMINARY; PRT; 176 AA.
AC Q9GKK2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell S.E., Nasir L., Argyle D.J., Gault E., Bennett D.;
RT "Canine IL-1 Receptor Antagonist cDNA Sequence.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216526; AG36777.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 176 AA; 19938 MW; 8486CA54A254206B CRC64;

```

```

Query Match 29.1%; Score 238; DB 6; Length 176;
Best Local Similarity 39.1%; Pred. No. 2.2e-17;
Matches 59; Conservative 20; Mismatches 62; Indels 10; Gaps 4;

QY 2 CSLPMARYIHKYADOKALYTRDQGLLVGDPVADNC-CAEKICTLPNRLDRTKVPFLG 60
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
33 CRMQAFRIWDV---NOKTYFLRNQLVAGYLOGSNTKLEKLDVPE-----PHAVFLG 84
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
61 IQGGSRLCLACVETEEGPSIQLEDVNIIEELKYGGEATRTFFQSSGSAFRLEAAWPGW 120
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
85 IHGGKICLACVKSGETRLQLEAVNTLDSKRNQKDRFTILSDSGPTTSFSAACPGW 144
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
121 FLCGPAEPPOPVOLTKSEPSAR-TKPYFEQ 150
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
145 FLCTALEADRLVSLTNRPPEAMWTKPYFOK 175

RESULT 11
ID Q9NZH8 PRELIMINARY; PRT; 169 AA.
AC Q9NZH8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN IL1E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

```

```

[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Grusold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT related protein 2: response is antagonized by IL-1d.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200492; AAF69248.1; -.
DR EMBL; AF206696; AAG35670.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Query Match 21.7%; Score 177.5; DB 4; Length 169;
Best Local Similarity 33.6%; Pred. No. 5.2e-11;
Matches 44; Conservative 21; Mismatches 61; Indels 5; Gaps 2;

QY 20 LYTRDQGLLVGDPVADNCCAEKI----CTLPNRLDRTKVPFLGIGGSRCLACVETE 75
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 34 VWTQGNLVAVPDSRDSVTPVTVAIVITKYPEALGGRGDPYILGIONPMLCYCEKVG 93
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 76 GPSIQLEDVNIIEELKYGGEATRTFFQSSGSAFRLEAAWPGWFLCGPAEPPOPVOLT 135
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 94 OPTLQLEKQIMDYGQPEVPKPFYRAKTGRTSTLESVAFPDWFIAS-SKRDQPIILT 152
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 136 KESEPSARTKF 146
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 153 SELGKSYNTAF 163

RESULT 12
ID Q9UHA5 PRELIMINARY; PRT; 157 AA.
AC Q9UHA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FIL1 ETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201833; AAF25213.1; -.
DR HSSP; P10749; 2M1B.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 157 AA; 17702 MW; 7A54F3D7557A3EE3 CRC64;

Query Match 21.5%; Score 176; DB 4; Length 157;
Best Local Similarity 36.6%; Pred. No. 6.8e-11;
Matches 34; Conservative 16; Mismatches 41; Indels 0; Gaps 0;

```

```
QY 57 IFGLGQSGRLACVETEEGSLQLEDVNIIEELYKGGEEATRTFTFFOSSGSAFRLAA 116
Db 62 VYLGIKGDGLCLFAEIQGKPTLQLKEKNIMDLVYKKAQKPFLLFFHNKKGSTSVFQSVS 121
QY 117 WPCWFLCGPAEPQPOPVOLTKTESPSARTKYFE 149
Db 122 YFCWFIATSTVSGOPIELTKERGITNTNTNYLD 154

RESULT 13
Q9D6Z6 PRELIMINARY; PRT; 183 AA.
AC Q9D6Z6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 2310043N20RIK PROTEIN.
CN 2310043N20RIK.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL: AK009787; BAB26505.1; -.
MGD; MGI:1916927; 2310043N20RIK.
InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;
```

```
Query Match 21.0%; Score 172; DB 11; Length 183;
Best Local Similarity 29.2%; Pred. No. 2.2e-10;
Matches 40; Conservative 25; Mismatches 68; Indels 4; Gaps 1;
```

```
QY 17 OKALYTRDQGLVGDVPADNCCAEKICTLPNRLDRTKVP-----IFGLGQSGRLACV 72
Db 44 QQWVWLVTGNTLTAVPASNVKPVILSLTACHDTEFDQVKGNLVFLGKNNRLCFCCVE 103
QY 73 TEEGSLQLEDVNIIEELYKGGEEATRTFTFFOSSGSAFRLAAAWPGLCPAEPQPOPV 132
Db 104 MEGKPTQLKQVDIMNLYKKAQKAFLLFYHGIEGSTSVFQSVLYPCWFIATSTIERQTI 163
QY 133 QLTKESEPSARTKYFE 149
Db 164 ILTHORGLVNTNYFE 180
```

```
RESULT 14
Q9UHA7 PRELIMINARY; PRT; 158 AA.
AC Q9UHA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FIL1 EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201831; AAF25211.1; -.
DR HSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
```

```
Query Match 20.7%; Score 169; DB 4; Length 158;
Best Local Similarity 32.0%; Pred. No. 3.8e-10;
Matches 40; Conservative 23; Mismatches 58; Indels 4; Gaps 1;
QY 26 QLLVGDVPADNCCAEKICTLPNRLDRTKV----PIFLGQSGRLACVETEEGSPSLQ 81
Db 28 QTLTAVPRKDRSPVTIALISCRHVSFTELEKDRGNPIYVLGLNGLNLCMAKVGDOPTQL 87
QY 82 EDVNIIEELYKGGEEATRTFTFFOSSGSAFRLAAAWPGLCPAEPQPOPVOLTKSEPS 141
Db 88 KKDMDLNLNQEPKVSFLFYHSGSGRSTFESVAFPGWFIASVSEGGCPILLTQELGKA 147
QY 142 ARTKF 146
Db 148 NTTDF 152
```

```
RESULT 15
Q7771 PRELIMINARY; PRT; 72 AA.
AC Q7771;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST SECRETORY FORM (FRAGMENT).
GN IL-1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRED THOROUGHBRED;
RA Dhar A.K., Thompson M.S., Paradis M.R., Alcivar-Warren A.;
RT "Molecular Characterization of Equine Interleukin 1 Receptor Antagonist (IL-1ra) Gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072476; AAC62237.1; -.
DR HSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 8215 MW; 290CC9B9D4C13D9 CRC64;
```







GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 07:54:55 ; Search time 270.73 seconds  
(without alignments)  
6468.632 Million cell updates/sec

Title: US-09-724-583-1  
Perfect score: 1020  
Sequence: 1 cagggtacgggttcagga.....acctctataaaaaaaaaa 1020

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SID55/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID55/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID55/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SID55/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SID55/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID55/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SID55/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SID55/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SID55/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SID55/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SID55/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SID55/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SID55/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SID55/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SID55/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SID55/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SID55/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SID55/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SID55/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID55/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	1020	22	Human interleukin-1
2	1016.8	99.7	1020	22	Human interleukin-1 rece
3	991.2	97.2	998	22	Human interleukin-
4	964.4	94.5	1366	22	Human interleukin-
5	964.4	94.5	1366	22	Human interleukin-
6	699.8	68.6	5445	22	Human interleukin-
7	657.6	64.5	744	22	Human interleukin-1 rece
8	634.8	62.2	827	22	Human IL-1 delta h
9	455.8	44.7	459	22	Human FIL-1 theta

10	412	40.4	483	22	AAF83868	Human interleukin-
11	368.4	36.1	538	22	AAD11158	Mouse FIL-1 theta
12	335.8	32.9	22	AAI70237	Human FIL-1 theta	
13	328.4	32.2	459	22	AAI70237	Mouse interleukin-
14	328.4	32.2	459	22	AAI70237	Mouse interleukin-
15	204.4	20.0	4388	22	AAI70237	Mouse interleukin-
16	204.4	20.0	13017	22	AAI70238	Mouse interleukin-
17	122.2	12.0	764	22	AH04444	Human CDNA clone (
18	117.8	11.5	562	22	AAI23955	Human breast cance
19	111.6	10.9	468	20	AAH89431	Mouse interleukin
20	111.6	10.9	468	22	AAI31373	Invention related
21	111.6	10.9	468	22	AAI31373	Murine interleukin
22	111.6	10.9	470	19	AAV71958	Rodent interleukin
23	111.6	10.9	1275	21	AAA09198	Murine IL-1 homolo
24	111.6	10.9	1284	22	AAI27924	Murine IL-1 codi
25	111.6	10.9	1360	21	AAZ50811	Murine TANGO-93 CD
26	111.6	10.9	1385	21	AAI51599	Murine IL-1 recept
27	110.8	10.9	488	20	AAH89432	Human interleukin
28	110.8	10.9	468	21	AAI51597	Human IL-1 recepto
29	110.8	10.9	766	21	AAI09193	Human IL-1 homolog
30	110.8	10.9	1025	22	AAI12295	Human interleukin-
31	110.8	10.9	1282	20	AAZ30050	CDNA encoding a hu
32	110.8	10.9	1282	22	AAI31353	Extension of B2HFL
33	110.8	10.9	1323	21	AAZ50812	Human TANGO-93 CDN
34	110.8	10.9	2490	21	AAZ50813	Human TANGO-93 CDN
35	110.8	10.9	2562	22	AAI27921	Human IL-1 codin
36	110.8	10.9	2598	22	AAI27921	Human IL-1 codin
37	110.8	10.9	2647	22	AAI31354	Extension of B2HFL
38	110.8	10.9	2648	20	AAZ30051	CDNA encoding a hu
39	108.8	10.7	1183	22	ABA06384	Human CDNA SEQ ID
40	108.8	10.7	1183	22	AAI29640	Human endocrine po
41	108.8	10.7	1183	22	AAI63963	Human polynucleoti
42	108.8	10.7	1183	22	AAI63963	Human CDNA encodin
43	108.8	10.7	1183	22	AAI63963	CDNA encoding nove
44	105.2	10.3	465	21	AAA09194	Human IL-1 homolog
45	105.2	10.3	465	21	AAA09195	Human IL-1 homolog

ALIGNMENTS

RESULT 1  
AAI70234  
ID AAI70234 standard: cDNA; 1020 BP.  
XX AC AAI70234;  
XX 07-JAN-2002 (first entry)  
XX Human interleukin-1 receptor antagonist related protein cDNA.  
XX Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;  
KW inhibitor; antiarthritic; antirheumatic; osteopathic;  
KW antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;  
KW antileptotic; antibacterial; tuberculostatic; anorectic; metabolic;  
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;  
KW antidepressant; anticonvulsive; tranquilizer; vulnerary;  
KW antiaesthetic; antipsoriatric; dermatologic; cytostatic;  
KW nephrotropic; antihemorrhagic; vasotrophic; cardiant;  
KW antithrombotic; antifertility; ophthalmological;  
KW gene therapy; diagnosis; ss.  
XX Homo sapiens.

Key	Location/Qualifiers
CDS	64..522
variation	/*tag= a replace(194,T)
variation	/*tag= b replace(215,C)
variation	/*tag= c

WC200142304-A1.





FH Key Location/Qualifiers  
FT CDS 54..512  
FT /\*tag= a  
FT /\*note= "encodes AAB19922"  
FT CDS 3..512  
FT /\*tag= b  
FT /\*partial  
FT /\*note= "alternative ORF, encodes AAB19923"  
FT variation replace(125,C)  
FT /\*tag= c  
FT /\*note= "alters codon GAT (Asp) to GAC (Asp),  
FT specifically claimed in Claim 9"  
FT variation replace(184,T)  
FT /\*tag= d  
FT /\*note= "alters codon ACA (Thr) to ATA (Ile),  
FT specifically claimed in Claim 9"  
FT variation replace(205,C)  
FT /\*tag= e  
FT /\*note= "alters codon GAC (Asp) to GCC (Ala),  
FT specifically claimed in Claim 9"  
XX WO200071719-A1.  
XX  
XX  
XX 30-NOV-2000.  
XX PD  
XX XX  
XX PF 22-MAY-2000; 2000WO-US14144.  
XX PR 20-MAY-1999; 99US-0316086.  
XX PR 10-MAR-2000; 2000US-0522964.  
XX XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;  
XX PI WPI; 2001-016409/02.  
XX DR P-PSDB; AAB19922, AAB19923.  
XX  
XX  
XX New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,  
XX preventing and treating disorders, such as cancers and inflammatory  
XX diseases -  
XX  
XX Claim 1; Page 128-130; 158pp; English.  
XX  
XX The present sequence is that of the cDNA insert of clone pIL-LH2  
XX (ATCC PTA-96) encoding human interleukin-1 Hy2 (IL-1 Hy2, see  
XX AAB19922 and AAB19923), a novel member of the interleukin-1 receptor  
XX antagonist family. The cDNA was obtained from a human foetal skin  
XX cDNA library using standard PCR, SBH sequence signature analysis  
XX and Sanger sequencing techniques. Sequencing of PCR products from  
XX various cDNA libraries revealed potential polymorphisms at  
XX nucleotides 125 (altering codon GAT to GAC, both Asp), 184  
XX (altering codon ACA for Thr to ATA for Ile) and 205 (altering  
XX codon GAC for Asp to GCC to Ala). 2 Alternative open reading  
XX frames were identified. The first had an initiating ATG codon at  
XX position 54-56 of the present sequence. However, a predicted cDNA  
XX sequence (see AA89178) based on IL-1 Hy2 genomic DNA contained a C  
XX to T change that resulted in an alternative upstream initiating  
XX methionine which extended the open reading frame. The IL-1 Hy2  
XX polypeptides and polynucleotides are used to treat cancers  
XX involving elevated levels of IL-1, such as breast adenocarcinoma,  
XX brain tumours, melanoma, giant cell tumours of bone, acute  
XX myelogenous leukaemia, oral epidermoid carcinoma or squamous cell  
XX carcinoma, and inflammatory disease mediated by interleukin-18 (all  
XX claimed). They can also be used to diagnose, prevent or treat  
XX shock, thrombosis, acute pancreatitis, arthritis, vasculitis,  
XX lupus, immune complex glomerulonephritis, pancreatic cell damage,  
XX allograft and xenograft transplantation, graft versus host disease,  
XX inflammatory bowel disease, bone degenerative diseases, diabetes  
XX and neurodegenerative disorders. The polynucleotides are also  
XX useful for the design of hybridization probes and PCR primers, in  
XX chromosome and gene mapping, in the recombinant production of  
XX IL-1 Hy2 protein, and in the generation of antisense DNA or RNA.

SQ Sequence 998 BP; 271 A; 236 C; 264 G; 227 T; 0 other;  
  
Query Match 97.2%; Score 991.2; DB 22; Length 998;  
Best Local Similarity 99.7%; Pred No. 2.1e-290;  
Matches 993; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 11 ggttcaggaaactcaggatctgcagtcgagtcagaccagaccacactgattgcaggaatgtgt 70  
Db 1 ggttcaggaaactcaggatctgcagtcgagtcagaccagaccacactgattgcaggaatgtgt 60  
  
Qy 71 cctctcccatgcaagatctacataataataatgcacacagagctctatcacaa 130  
Db 61 cctctcccatgcaagatctacataataataatgcacacagagctctatcacaa 120  
  
Qy 131 gagatggccagctgctggtggagatcctgttcagacaactgctgtgcagagaagatct 190  
Db 121 gagatggccagctgctggtggagatcctgttcagacaactgctgtgcagagaagatct 180  
  
Qy 191 qcacacttcttaacagagcttgaccgcacccaaggtccccaatttctcggggacagg 250  
Db 181 qcacacttcttaacagagcttgaccgcacccaaggtccccaatttctcggggacagg 240  
  
Qy 251 gagggagccgctgctggtgcagtgtgtggagacagaagaggccctccctacagctggagg 310  
Db 241 gagggagccgctgctggtgcagtgtgtggagacagaagaggccctccctacagctggagg 300  
  
Qy 311 atgtgaacattgagaaactgtacaaaggtggtgaagagccacagcttcacctctcc 370  
Db 301 atgtgaacattgagaaactgtacaaaggtggtgaagagccacagcttcacctctcc 360  
  
Qy 371 agagcagctcaggctccgcttcaggcttgagctgctgctgctgctgctgctgctgctgt 430  
Db 361 agagcagctcaggctccgcttcaggcttgagctgctgctgctgctgctgctgctgt 420  
  
Qy 431 gtggtccggtcagagcccgagcagccagtcacagctcccaagagagagtcctcagcccc 490  
Db 421 gtggtccggtcagagcccgagcagccagtcacagctcccaagagagagtcctcagcccc 480  
  
Qy 491 gtaccagaatttactttgaacagagctggttagggagacaggaactcggttttagccttg 550  
Db 481 gtaccagaatttactttgaacagagctggttagggagacaggaactcggttttagccttg 540  
  
Qy 551 tgcctcccaacaaagctcatctcctcaggtgtctatgtaggcagaataatgtcccccg 610  
Db 541 tgcctcccaacaaagctcatctcctcaggtgtctatgtaggcagaataatgtcccccg 600  
  
Qy 611 aatatgtccacatccttaataccagagctgtgcataatgttaccatacatgtccaaaagg 670  
Db 601 aatatgtccacatccttaataccagagctgtgcataatgttaccatacatgtccaaaagg 660  
  
Qy 671 ttttgcaaatgtgattatgttaagatcttgaagtgcagagacaaactcctggtttatcctt 730  
Db 661 ttttgcaaatgtgattatgttaagatcttgaagtgcagagacaaactcctggtttatcctt 720  
  
Qy 731 gtgggtcagtttaataccagagagagggcaggaagggagagtcagagagaagaatggaag 790  
Db 721 gtgggtcagtttaataccagagagagggcaggaagggagagtcagagagaagaatggaag 780  
  
Qy 791 ataccatgcttctaattttgaagatggagtgcagggccttgagcccaaaatgcaggtgt 850  
Db 781 ataccatgcttctaattttgaagatggagtgcagggccttgagcccaaaatgcaggtgt 840  
  
Qy 851 ttttagaagggtgaaaagcccaagggagcgatctctctctagatgctccggaaggaacac 910  
Db 841 ttttagaagggtgaaaagcccaagggagcgatctctctctctagatgctccggaaggaacac 900  
  
Qy 911 agctcttgacacatgatttcagctcagtcagtcacccatttcagacttctgacctcccaa 970  
Db 901 agctcttgacacatgatttcagctcagtcagtcacccatttcagacttctgacctcccaa 960  
  
Qy 971 ctataaaataaaactgtgttattgtaaacctct 1006  
|||||



RESULT	5
AAA89178	
ID	AAA89178 standard; cDNA; 1366 BP.
XX	
AC	AAA89178;
XX	
DT	19-MAR-2001 (first entry)
XX	
DE	Human interleukin-1 Hy2 cDNA (alternative ORF).
XX	
KW	Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW	antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW	myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW	oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW	antitumour; antinflammatory; diagnosis; therapy; chromosome 2; ss.
XX	
OS	Homo sapiens.
Key	Location/Qualifiers
CDS	278..880
FT	/*tag= a
XX	
PN	WO200071719-A1.
XX	
PD	30-NOV-2000.
XX	
PF	22-MAY-2000; 2000WO-US14144.
XX	
PR	20-MAY-1999; 99US-0316086.
PR	10-MAR-2000; 2000US-0522964.
XX	
PA	(HYSE-) HYSEQ INC.
PI	Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;
XX	
DR	WPI; 2001-016409/02.
DR	P-PSDB; AAB19924.
PT	New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT	preventing and treating disorders, such as cancers and inflammatory
PT	diseases -
XX	
PS	Claim 1; Page 143; 158pp; English.
XX	
CC	The present sequence is that of cDNA encoding human interleukin-1
CC	Hy2 (IL-1 Hy2, see AAB19924), a novel member of the interleukin-1
CC	receptor antagonist family. The sequence was deduced from isolated
CC	IL-1 Hy2 genomic DNA (see AAA89177). It contains thymidine at
CC	nucleotide 279, whereas IL-1 Hy2 cDNA obtained by PCR amplification
CC	(see AAA89176) has cytosine at this position. The C to T change
CC	extends the IL-1 Hy2 open reading frame in the 5' direction.
CC	resulting in a 200-amino acid protein, while the amplified cDNA
CC	encodes a 152-amino acid protein (see AAB19922). However, sequences
CC	surrounding the translation initiation codon at nucleotide 422 of
CC	the present sequence are more similar to the Kozak translation
CC	start site consensus than the sequences surrounding nucleotide 278,
CC	suggesting that IL-1 Hy2 is encoded by the shorter open reading
CC	from. IL-1 Hy2 polypeptides and polynucleotides are used to treat
CC	cancers involving elevated levels of IL-1, such as breast
CC	adenocarcinoma, brain tumours, melanoma, giant cell tumours of
CC	bone, acute myelogenous leukaemia, oral epidermoid carcinoma or
CC	squamous cell carcinoma, and inflammatory disease mediated by
CC	interleukin-18 (all claimed). They can also be used to diagnose,
CC	prevent or treat shock, thrombosis, acute pancreatitis, arthritis,
CC	vascutitis, lupus, immune complex glomerulonephritis, pancreatic
CC	cell damage, allograft and xenograft transplantation, graft versus
CC	host disease, inflammatory bowel disease, bone degenerative
CC	diseases, diabetes and neurodegenerative disorders. The
CC	polynucleotides are also useful for the design of hybridization
CC	probes and PCR primers, in chromosome and gene mapping, in the
CC	recombinant production of IL-1 Hy2 protein, and in the generation
CC	of antisense DNA or RNA.



Qy 956 ttctgacctcacactataaaataaactgtgttattgtaaacctt 1006  
Db 5395 ttctgacctcacactataaaataaactgtgttattgtaaacctt 5445

RESULT 7  
AAI70236  
ID AAI70236 standard; cDNA; 744 BP.  
AC AAI70236;  
XX  
XX 07-JAN-2002 (first entry)  
DE Interleukin-1 receptor antagonist related protein splice variant.  
XX  
XX Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;  
KW inhibitor; antiarthritic; antirheumatic; osteopathic;  
KW antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;  
KW antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;  
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;  
KW antidepressant; anticonvulsive; tranquilizer; cytostatic;  
KW antitachycardic; antihemorrhagic; vasotropic; cardiac;  
KW antithrombotic; antinfertility; ophthalmological;  
KW gene therapy; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 58..573 /\*tag= a  
XX  
XX W0200142304-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 04-DEC-2000; 2000WO-US32940.  
XX  
XX 10-DEC-1999; 99US-170191P.  
XX 09-MAR-2000; 2000US-188053P.  
XX 04-APR-2000; 2000US-194521P.  
XX 10-APR-2000; 2000US-195910P.  
XX 28-NOV-2000; 2000US-0170191.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Saris CM, Giles J, Mu SX, Xia M, Bass MB, Craveiro R;  
XX WPI; 2001-648140/74.  
XX P-PSDB; AAM50219.  
XX  
XX Novel interleukin-1 receptor antagonist-related polypeptide, its  
XX fragment, variant useful for treating rheumatoid arthritis, septicemia,  
XX Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,  
XX uveitis, eczema  
XX  
XX Claim 1; Fig 3; 163pp; English.  
XX  
XX The present sequence is that of cDNA encoding a splice variant (see  
XX AAM50219), of human interleukin-1 receptor antagonist-related  
XX polypeptide IL-1ra-R, a novel protein that has interleukin-1  
XX inhibitor activity. The sequence was obtained from a human  
XX placenta cDNA library by PCR amplification. The splice variant  
XX may arise from splicing (or a fusion) of the first 2 exons of  
XX the upstream IL-1 Omega gene onto the second exon of the IL-1ra-R  
XX gene. The invention provides IL-1ra-R polypeptides and nucleic  
XX acids, as well as selective binding agents, vectors, host cells  
XX and methods for producing the IL-1ra-R polypeptides. It also  
XX provides pharmaceutical compositions and methods for the diagnosis,  
XX treatment, amelioration and/or prevention of diseases, disorders  
XX and conditions associated with IL-1ra-R, such as those involving  
XX immune system dysfunction, infection, weight disorders, neuronal

CC dysfunction, lung, skin, kidney, bone, vascular system, tumour  
CC cells, reproductive system, and eye. The nucleic acids are useful  
CC in gene therapy, gene mapping, transgenic animal breeding, and as  
CC probes and primers.  
XX  
SQ Sequence 744 BP; 183 A; 194 C; 205 G; 162 T; 0 other;  
  
Query Match 64.5%; Score 657.6; DB 22; Length 744;  
Best Local Similarity 99.4%; Pred. No. 3.6e-189;  
Matches 660; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 30 ctgcagtgaggaccagacacacactgattgcaggaaatgtttccctcccatggccaagata 89  
Db 81 ctctccctgaggaccagacacacactgattgcaggaaatgtttccctcccatggccaagata 140  
Qy 90 ctacataataaataatgcagaccagaaggctctacacagaagatgccagctgctggt 149  
Db 141 ctacataataaataatgcagaccagaaggctctacacagaagatgccagctgctggt 200  
Qy 150 gggagatcctgttcagacaactctgtgcagagaagatctgcacacttcttaacagag 209  
Db 201 gggagatcctgttcagacaactctgtgcagagaagatctgcacacttcttaacagag 260  
Qy 210 cttggaccgcacaaaggctcccatcttctggggatccaggaggagcgctgcctggc 269  
Db 261 cttggccgcacaaaggctcccatcttctggggatccaggaggagcgctgcctggc 320  
Qy 270 atgtgtggagacagagaggggccttccctacagctggaggatggaacattgaggaa 329  
Db 321 atgtgtggagacagagaggggccttccctacagctggaggatggaacattgaggaa 380  
Qy 330 gtacaaagggtggtgaagaggccacgccttccctacagctgcttcacagagcagctcgc 389  
Db 381 gtacaaagggtggtgaagaggccacgccttccctacagctgcttcacagagcagctcgc 440  
Qy 390 cttcaggcttgaggctgctgctgctgctgctgctgctgctgctgctgctgctgctg 449  
Db 441 cttcaggcttgaggctgctgctgctgctgctgctgctgctgctgctgctgctgctg 500  
Qy 450 gcagccagtacagctcaccagaggagagtgagccctcagccctaccagtttacttga 509  
Db 501 gcagccagtacagctcaccagaggagtgagccctcagccctaccagtttacttga 560  
Qy 510 acagagctgtgaggagacaggaactgcgttttagcctgtgcccccaaaccaagctca 569  
Db 561 acagagctgtgaggagacaggaactgcgttttagcctgtgcccccaaaccaagctca 620  
Qy 570 tctgtctcagggtctatggtgaggcagaataatgtcccccgaaatatgtccacatcctaa 629  
Db 621 tctgtctcagggtctatggtgaggcagaataatgtcccccgaaatatgtccacatcctaa 680  
Qy 630 cccaagatctgtcatatgttaccatatactgtccaaagagggttttgcaaatgtgattatg 689  
Db 681 cccaagatctgtcatatgttaccatatactgtccaaagagggttttgcaaatgtgattatg 740  
Qy 690 ttaa 693  
Db 741 ttaa 744  
  
RESULT 8  
ABA08991  
ID ABA08991 standard; cDNA; 827 BP.  
AC ABA08991;  
XX  
XX 11-JAN-2002 (first entry)  
XX  
XX Human IL-1 delta homologue-encoding cDNA, SEQ ID NO:767.  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;





DE Human FIL-1 theta full-length DNA..

XX Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;

XX insulin dependent diabetes mellitus; lymphoma; microbial infection;

KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;

KW tibial muscular dystrophy; inflammation; gene therapy; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

PH 1..459

FT /\*tag= a

FT /product= "Human FIL-1 theta full-length protein"

FT replace (131, T)

FT /\*tag= b

FT /note= "This polymorphism results in an amino

FT acid change from Thr to Ile at position 44"

FT replace (131..132, TC)

FT /\*tag= b

FT /note= "This polymorphism results in an amino

FT acid change from Thr to Ile at position 44"

FT replace (152, C)

FT /\*tag= b

FT /note= "This polymorphism results in an amino

FT acid change from Asp to Ala at position 51"

XX WO200155211-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02514.

XX 27-JAN-2000; 2000US-0178389.

XX 11-APR-2000; 2000US-0195962.

XX (IMMUNEX CORP.

XX SIMS JE;

XX WPI: 2001-457718/49.

XX P-PSDB; AAE05840.

XX Isolated FIL-1 theta polypeptide to induce or inhibit the induction of

XX fever and to stimulate the immune system for the treatment of microbial

XX infections -

XX Claim 1; Page 5; 65pp; English.

XX The invention relates to interleukin-1 (IL-1) family ligand designated

XX as FIL-1 theta polypeptides and nucleic acid molecules encoding such

XX polypeptides. Fil-1 theta DNA is used to identify glaucoma, insulin

XX dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/

XX lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. Fil-1

XX theta polypeptides are used to activate and/or inhibit the activation

XX of vascular endothelial cells and lymphocytes; the induction of local

XX tissue destruction and fever; the stimulation of macrophages and

XX vascular endothelial cells to produce IL-6 and the induction of

XX prostaglandins. They are also used to treat inflammation and microbial

XX infections. FIL-1 theta DNA is useful in antisense therapy and gene

XX therapy. The present sequence is a DNA encoding human FIL-1 theta

XX full-length protein.

XX Sequence 459 BP; 109 A; 124 C; 132 G; 94 T; 0 other;

Query Match 44.7%; Score 455.8; DB 22; Length 459;

Best Local Similarity 99.6%; Pred. No. 5.2e-128;

Matches 457; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 atgtgttccctcccccgaagatgactacataataataatgacagcagaaggtcta 123

DB 1 atgtgttccctcccccgaagatgactacataataataatgacagcagaaggtcta 60

QY 124 tacacagagatggccagctgctggtgggagatcctgttgcagacacaaactggtgcagag 183

DB 61 tacacagagatggccagctgctggtgggagatcctgttgcagacacaaactggtgcagag 120

QY 184 aagatctgcacacttctaacagagcttgagccgaccaaaggtcccatcttctctggg 243

DB 121 aagatctgcacacttctaacagagcttgagccgaccaaaggtcccatcttctctggg 180

QY 244 atccagagagagagccgctgctgcctgcatgtgtgagacagagaagggccttccctacag 303

DB 181 atccagagagagagccgctgctgcctgcatgtgtgagacagagaagggccttccctacag 240

QY 304 ctggagatgtgaacttgaggaaactgtacaaaggtggtgaagagggccacacgcttccac 363

DB 241 ctggagatgtgaacttgaggaaactgtacaaaggtggtgaagagggccacacgcttccac 300

QY 364 tcttccagagcagctcaggtccgccttcaggtctgaggtgctgctgctgctgctgctg 423

DB 301 tcttccagagcagctcaggtccgccttcaggtctgaggtgctgctgctgctgctgctg 360

QY 424 tctctgtgtggccgagcagagccagcagcagcagcagcagcagcagcagcagcagcagc 483

DB 361 tctctgtgtggccgagcagagccagcagcagcagcagcagcagcagcagcagcagcagc 420

QY 484 tcagccgctaccagtttactttactttgaacagagctggtag 522

DB 421 tcagccgctaccagtttactttactttgaacagagctggtag 459

RESULT 10

AAF83868

ID AAF83868 standard; cDNA; 483 BP.

XX

AC AAF83868;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human interleukin-1 receptor antagonist (NOVINTRA A) encoding cDNA.

XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;

XX gonadotropin-like protein; NOVCON; interleukin-1; NOVINTRA; human;

XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;

XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;

XX antiasthmatic; antiallergic; ss.

XX Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 3..467

FT /\*tag= a

FT /product= "NOVINTRA A"

XX

PN WO200140291-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US33029.

XX

PR 06-DEC-1999; 99US-0169056.

PR 09-DEC-1999; 99US-0169866.

PR 09-DEC-1999; 99US-0169886.

PR 10-DEC-1999; 99US-0170252.

PR 12-JAN-2000; 2000US-0175740.

PR 05-DEC-2000; 2000US-0170252.

XX

XX (CURA-) CURAGEN CORP.

PA

XX Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;

PI Mezes PS;

XX

XX WPI: 2001-374790/39.

DR P-PSDB; AAB84999.

XX

PT Novel isolated human transmembrane, neuromedin peptide  
PT gonadotropin-like protein and interleukin-1 receptor antagonist  
PT proteins, useful for treating cancer, immune response disorder,  
PT metabolic function disorders  
XX  
PS Claim 8; Fig 9A; 138pp; English.  
XX  
CC The invention provides novel polypeptides (NOVX) selected from human  
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
CC antagonist proteins (NOVINTRA A and B). The invention also provides  
CC methods in which a NOVX polypeptide, polynucleotide and antibody are  
CC used in the detection, prevention and treatment of a broad range of  
CC pathological states. NOVTRAN can be used to treat a cell signaling  
CC disorder such as cancer, immune response disorder, hematopoietic  
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
CC central nervous system, breast, colon, ovary, kidney, prostate and  
CC thyroid. NOVGON can be used to treat reproductive development disorder,  
CC metabolic function disorder and melanoma. NOVINTR A and B can be used  
CC to treat bone metabolism or structure disorder, inflammatory response  
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
CC arthritis and cancer. The present sequence represents a cDNA encoding  
CC the NOVINTR A polypeptide.

XX Sequence 483 BP; 114 A; 134 C; 138 G; 97 T; 0 other;

Query Match 40.4%; Score 412; DB 22; Length 483;  
Best Local Similarity 93.5%; Pred. No. 1,le-114;  
Matches 449; Conservative 0; Mismatches 10; Indels 21; Gaps 1;

Qy 80 tggcagatgactacataataatgacagacagagaggtctctacacagagatgccc 139  
Db 4 tgtcactgtttcagaataatgacagacagagaggtctctacacagagatgccc 63  
Qy 140 agctgtctgtggagatcctgtgcagacaaactgtgtgcagagagatctgcacacttc 199  
Db 64 agctgtctgtggagatcctgtgcagacaaactgtgtgcagagagatctgcacacttc 123  
Qy 200 ctacagagcttgacccagcagcaaggtcccatcttctgtggatccagagagagcc 259  
Db 124 ctacagagcttgacccagcagcaaggtcccatcttctgtggatccagagagagcc 183  
Qy 260 gctgctgtgcatgtgtgagacagagaggggcccctccctcacagtgg----- 307  
Db 184 gctgctgtgcatgtgtgagacagagaggggcccctccctcacagtggagccacact 243  
Qy 308 -----aggatgtgacattgaggaactgtacaaagggtgtgaagagggcacacgct 358  
Db 244 tgcctccacagagatgtgacattgaggaactgtacaaagggtgtgaagagggcacacgct 303  
Qy 359 tcactcttccagagagctcaggtccgccttcaggtctgaggtgctgctgctgctg 418  
Db 304 tcactcttccagagagctcaggtccgccttcaggtctgaggtgctgctgctgctg 363  
Qy 419 gctggttctgtgtgcccgcagagagcccccagcagcagtcagtcacacagagagtg 478  
Db 364 gctggttctgtgtgcccgcagagagcccccagcagcagtcagtcacacagagagtg 423  
Qy 479 agcctcagccgctaccagtttactttgaacagagctgtgagagagagagaaactgc 538  
Db 424 agcctcagccgctaccagtttactttgaacagagctgtgagagagagagaaactgc 483

RESULT 11

AD11158  
ID AD11158 standard; DNA; 538 BP.

XX  
AC AD11158;

XX  
DT 24-SEP-2001 (first entry)

DE Mouse FIL-1 theta DNA.  
XX  
KW Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;  
KW insulin dependent diabetes mellitus; lymphoma; microbial infection;  
KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;  
KW tibial muscular dystrophy; inflammation; gene therapy; mouse; ds.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 29..487  
FT /\*tag= a  
FT /product= "Mouse FIL-1 theta protein"  
PN W0200155211-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02514.  
XX  
PR 27-JAN-2000; 2000US-0178389.  
PR 11-APR-2000; 2000US-0195962.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Sims JE;  
XX  
XX WPI; 2001-457718/49.  
XX P-PSDB; AAE05841.  
XX  
XX Isolated FIL-1 theta polypeptide to induce or inhibit the induction of  
XX fever and to stimulate the immune system for the treatment of microbial  
XX infections -  
XX  
PS Claim 1; Page 5-6; 65pp; English.  
XX  
CC The invention relates to interleukin-1 (IL-1) family ligand designated  
CC as FIL-1 theta polypeptides and nucleic acid molecules encoding such  
CC polypeptides. Fil-1 theta DNA is used to identify glaucoma, insulin  
CC dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/  
CC lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. Fil-1  
CC theta polypeptides are used to activate and/or inhibit the activation  
CC of vascular endothelial cells and lymphocytes; the induction of local  
CC tissue destruction and fever; the stimulation of macrophages and  
CC vascular endothelial cells to produce IL-6 and the induction of  
CC prostaglandins. They are also used to treat inflammation and microbial  
CC infections. FIL-1 theta DNA is useful in antisense therapy and gene  
CC therapy. The present sequence is a DNA encoding mouse FIL-1 theta  
CC protein.  
XX  
SQ Sequence 538 BP; 132 A; 148 C; 140 G; 118 T; 0 other;

Query Match 36.1%; Score 368.4; DB 22; Length 538;  
Best Local Similarity 80.3%; Pred. No. 2e-101;  
Matches 432; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 36 ttgagacagacacacactgattgacaggaatgtgttccctcccatggcagatactacat 95  
Db 1 tgaagacagacacactcccaactgacaggaatgtgttccctcccatggcagatactacat 60  
Qy 96 aatcaaatatgcagacagagctctctacacagagatggccagctgctggtggaga 155  
Db 61 aatcaagatgcacatacaaaaggctttgtacacacggaatggccagctgctggtggaga 120  
Qy 156 tctctgttcacacactgctgtgcagagaagatctgcacacttccctaaagagcttga 215  
Db 121 cctgattcagacaaatattagtcacagagaaggtctgtatcttcttaaccagagcctaga 180  
Qy 216 ccgcaccaaggtcccccatttctctggggatccagggagagccgctgctgctgctgctgt 275  
Db 181 ccgctccaaggtcccccatttctctggggatccagggagaggaagtgtgctgctgctgctgt 240



PR 28-NOV-2000; 2000US-0170191.  
 XX (AMGE-) AMGEN INC.  
 PA Saris CM, Giles J, Mu SX, Xia M, Bass MB, Craveiro R;  
 PI  
 XX WPI: 2001-648140/74.  
 DR P-PSDB; AAM50220.  
 XX  
 PT Novel interleukin-1 receptor antagonist-related polypeptide, its  
 fragment, variant useful for treating rheumatoid arthritis, septicemia,  
 PT Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,  
 PT uveitis, eczema  
 XX  
 PS Claim 1; Fig 7; 163pp; English.  
 XX  
 CC The present sequence is that of the coding region of cDNA encoding a  
 CC novel murine interleukin-1 receptor antagonist-related polypeptide,  
 CC IL-1ra-R (see AAM50220), which has interleukin-1 inhibitor activity.  
 CC The cDNA was obtained from a day 7 mouse embryo cDNA library. The  
 CC mouse IL-1ra-R gene sequence was also determined (see AAI70238).  
 CC The invention provides mouse and human IL-1ra-R polypeptides and  
 CC nucleic acids, as well as selective binding agents, vectors, host  
 CC cells and methods for producing the IL-1ra-R polypeptides. It also  
 CC provides pharmaceutical compositions and methods for the diagnosis,  
 CC treatment, amelioration and/or prevention of diseases, disorders  
 CC and conditions associated with IL-1ra-R, such as those involving  
 CC immune system dysfunction, infection, weight disorders, neuronal  
 CC dysfunction, lung, skin, kidney, bone, vascular system, tumour  
 CC cells, reproductive system, and eye. The nucleic acids are useful  
 CC in gene therapy, gene mapping, transgenic animal breeding, and as  
 CC probes and primers.  
 XX  
 SQ Sequence 459 BP; 113 A; 125 C; 119 G; 102 T; 0 other;

Query Match 32.2%; Score 328.4; DB 22; Length 459;  
 Best Local Similarity 82.3%; Pred. No. 2.5e-89;  
 Matches 377; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 64 atgtgtctccctccatggaagataactacataataataatcagaccagaagctcta 123  
 Db 1 atgtgtctccctccatggaagataactacataataataatcagaccagaagcttg 60  
 Qy 124 tacacaagagatggcagctgctgtggagatcctgttgcagacaactgtgtgcagag 183  
 Db 61 tacacaggaatggcagctgctgtggagacccctgtattcagacaattatagtcagag 120  
 Qy 184 aagatctgcacactctcctaagcagagctgtggaccgacacaggtcccccatttctctgggg 243  
 121 aaggtctgtatctctcctaagcagagctgtggaccgacacaggtcccccatttctctgggg 180  
 Qy 244 atccagggaggagcgctgctgtgcatgtgtggagacagagagggccttccctacag 303  
 Db 181 atcagggaggagagtgctgtgctgtgtgttaagacagagagagggacctctctctgcag 240  
 Qy 304 ctgagagatgtgaacatgtggaactgtacaaaggtgtggaagggccacagccttccacc 363  
 Db 241 ctgagagatgtgaacatgtggaactgtacaaagggaggtgacaaacccctttccacc 300  
 Qy 364 ttctccagagcagctcaggtccgcttccagcttgcagctgtgagctgtgctgtgctgtg 423  
 Db 301 ttctccagagcagcttggatctgcttccagcttgcagctgtgagctgtgctgtgctgtg 360  
 Qy 424 ttctctgtgtgcccagagccccacagccagctacagctcacaagagagatgagccc 483  
 Db 361 ttctctgtgtgcccagagctgagccccagcagctgagctgagctgagctgagctgagccc 420  
 Qy 484 tcagcccgtaaccaagttttactttgaacagagctgcta 521  
 Db 421 tccaccactactgaattctactttgagatgagtcgta 458

RESULT 14  
 AAA89180  
 ID AAA89180 standard; cDNA; 459 BP.  
 XX  
 AC AAA89180;  
 XX  
 DT 19-MAR-2001 (first entry)  
 DE Mouse interleukin-1 Hy2 cDNA.  
 XX  
 KW Interleukin-2 Hy2; IL-1 Hy2; mouse; interleukin-1 receptor;  
 KW antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;  
 KW myeloma; giant cell tumour of bone; acute myelogenous leukaemia;  
 KW oral epidermoid carcinoma; squamous cell carcinoma; inflammation;  
 KW antitumour; antiinflammatory; diagnosis; therapy; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200071719-A1.  
 XX  
 PD 30-NOV-2000.  
 XX  
 PF 22-MAY-2000; 2000WO-US14144.  
 XX  
 PR 20-MAY-1999; 99US-0316086.  
 PR 10-MAR-2000; 2000US-0522964.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;  
 XX  
 DR WPI: 2001-016409/02.  
 DR P-PSDB; AAB19925.  
 XX  
 PT New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,  
 PT preventing and treating disorders, such as cancers and inflammatory  
 PT diseases -  
 XX  
 PS Example 9; Page 152; 158pp; English.  
 XX  
 CC The present sequence is that of mouse cDNA encoding interleukin-1 Hy2  
 CC (IL-1 Hy2; see AAB19925), a novel member of the interleukin-1 receptor  
 CC antagonist family. The sequence is predicted from isolated IL-1 Hy2  
 CC genomic DNA (see AAB19925). The predicted mouse and human (see  
 CC AAB19922) IL-1 Hy2 polypeptides share 81.7% homology. The murine  
 CC genomic DNA can be used to generate transgenic animals which overexpress  
 CC IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out. Human  
 CC IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers  
 CC involving elevated levels of IL-1, such as breast adenocarcinoma,  
 CC brain tumours, melanoma, giant cell tumours of bone, acute  
 CC myelogenous leukaemia, oral epidermoid carcinoma or squamous cell  
 CC carcinoma, and inflammatory disease mediated by interleukin-18 (all  
 CC claimed).  
 XX  
 SQ Sequence 459 BP; 113 A; 125 C; 119 G; 102 T; 0 other;

Query Match 32.2%; Score 328.4; DB 22; Length 459;  
 Best Local Similarity 82.3%; Pred. No. 2.5e-89;  
 Matches 377; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 64 atgtgtctccctccatggaagataactacataataataatcagaccagaagctcta 123  
 Db 1 atgtgtctccctccatggaagataactacataataataatcagaccagaagcttg 60  
 Qy 124 tacacaagagatggcagctgctgtggagatcctgttgcagacaactgtgtgcagag 183  
 Db 61 tacacaggaatggcagctgctgtggagacccctgtattcagacaattatagtcagag 120  
 Qy 184 aagatctgcacactctcctaagcagagctgtggaccgacacaggtcccccatttctctgggg 243  
 Db 121 aaggtctgtatctctcctaagcagagctgtggaccgacacaggtcccccatttctctgggg 180

